

164213

From: Mertz, Prema
Sent: Monday, August 29, 2005 2:48 PM
To: STIC-Biotech/ChemLib
Subject: 10/649,857

Please search SEQ ID NO:45 with protein databases.

Thanks

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STAFF USE ONLY

Searcher: _____
Searcher Phone: 2-
Date Searcher Picked Up: *08/29/05*
Date Completed: *08/29/05*
Searcher Prep/Rev. Time: _____
Online Time: _____

Type of Search

NA#: _____ AA#: *1*
Interference: _____ SPDI: _____
S/L: _____ Oligomer: _____
Encode/Transl: _____
Structure#: _____ Text: _____
Inventor: _____ Litigation: _____

Vendors and cost where applicable

STN: _____
DIALOG: _____
QUESTEL/ORBIT: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: *08/29/05*
WWW/Internet: _____
Other(Specify): _____

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OM protein - protein search, using sw model

Run on: August 29, 2005 20:32:38 ; Search time 162 Seconds

(without alignments)

162.507 Million cell updates/sec

Title: US-10-649-857-45

Perfect score: 371

Sequence: 1 MGRCICRGAEISLCSFSEFPL.....PGTPRAFGLFLIFESFWAV 67

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1767149 seqs, 392926209 residues

Total number of hits satisfying chosen parameters: 1767149

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Published Applications AA:*

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4: /cgn2_6/ptodata/2/pubpaas/us06_PUBCOMB.pep:*

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19: /cgn2_6/ptodata/2/pubpaas/us11_NBW_PUBCOMB.pep:*

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RESULT 1

US-09-814-122-45

; Sequence 45, Application US/09814122

; Patent No. US20020058307A1

; GENERAL INFORMATION:

; APPLICANT: Craig Rosen et al.

; TITLE OF INVENTION: 20 Human Secreted Proteins

; FILE REFERENCE: PZ0051

; CURRENT APPLICATION NUMBER: US/09/814,122

; CURRENT FILING DATE: 2001-03-22

; EARLIER APPLICATION NUMBER: US/09/166,780

; EARLIER FILING DATE: 1998-10-06

; EARLIER APPLICATION NUMBER: PCT/US98/06801

; EARLIER FILING DATE: 1998-04-07

; EARLIER APPLICATION NUMBER: 60/042,726

; EARLIER APPLICATION NUMBER: 60/042,727

; EARLIER FILING DATE: 1997-04-08

; EARLIER APPLICATION NUMBER: 60/042,728

; EARLIER FILING DATE: 1997-04-08

; EARLIER APPLICATION NUMBER: 60/042,754

; EARLIER FILING DATE: 1997-04-08

; EARLIER APPLICATION NUMBER: 60/042,825

; EARLIER FILING DATE: 1997-04-08

; EARLIER APPLICATION NUMBER: 60/048,068

; EARLIER FILING DATE: 1997-05-30

; EARLIER APPLICATION NUMBER: 60/048,070

; EARLIER FILING DATE: 1997-05-30

; EARLIER APPLICATION NUMBER: 60/048,184

; EARLIER FILING DATE: 1997-05-30

; NUMBER OF SEQ ID NOS: 86

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 45

; LENGTH: 67

ALIGNMENTS

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APPLICANT: La Rossa, Thomas J.
 APPLICANT: Kovacic, David K.
 APPLICANT: Zhou, Yihua
 APPLICANT: Cao, Yongwei
 TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
 FILE REFERENCE: 38-21(53222)B
 CURRENT APPLICATION NUMBER: US/10/425,115
 NUMBER OF SEQ ID NOS: 369326
 SEQ ID NO 316330
 LENGTH: 98
 TYPE: PRT
 ORGANISM: zea mays
 FEATURE:
 NAME/KEY: unsure
 LOCATION: (1) .(98)
 OTHER INFORMATION: unsure at all Xaa locations
 OTHER INFORMATION: Clone ID: MRT4577_5156IC.1.pep
 US-10-425-115-316330

Query Match 100.0%; Score 371; DB 9; Length 67;
 Best Local Similarity 100.0%; Pred. No. 6.2e-34;
 Matches 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGKCLRGAEELSLCFSFPPLPLHPTVAGRNGLGPBESLGVPPFLPHPGTTPRAPGFLLL 60
 Db 1 MGKCLRGAEELSLCFSFPPLPLHPTVAGRNGLGPBESLGVPPFLPHPGTTPRAPGFLLL 60

Qy 61 LPSFWAV 67
 Db 61 LPSFWAV 67

RESULT 2
 US-10-649-857-45
 Sequence 45, Application US/10649857
 Publication No. US20040063128A1
 GENERAL INFORMATION:
 APPLICANT: Craig Rosen et al.
 TITLE OF INVENTION: 20 Human Secreted Proteins
 FILE REFERENCE: P2005PP
 CURRENT APPLICATION NUMBER: US/10/649,857
 PRIOR APPLICATION NUMBER: US/09/166,780
 PRIOR FILING DATE: 2003-08-28
 PRIOR APPLICATION NUMBER: US/09/166,780
 PRIOR FILING DATE: 1998-10-06
 PRIOR APPLICATION NUMBER: PCT/US98/06801
 PRIOR FILING DATE: 1998-04-07
 PRIOR APPLICATION NUMBER: 60/042,726
 PRIOR FILING DATE: 1997-04-08
 PRIOR APPLICATION NUMBER: 60/042,727
 PRIOR FILING DATE: 1997-04-08
 PRIOR APPLICATION NUMBER: 60/042,728
 PRIOR FILING DATE: 1997-04-08
 PRIOR APPLICATION NUMBER: 60/042,754
 PRIOR FILING DATE: 1997-04-08
 PRIOR APPLICATION NUMBER: 60/042,825
 PRIOR FILING DATE: 1997-04-08
 PRIOR APPLICATION NUMBER: 60/048,068
 PRIOR FILING DATE: 1997-05-30
 PRIOR APPLICATION NUMBER: 60/048,070
 PRIOR FILING DATE: 1997-05-30
 PRIOR APPLICATION NUMBER: 60/048,184
 PRIOR FILING DATE: 1997-05-30
 NUMBER OF SEQ ID NOS: 86
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO 45
 LENGTH: 67
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-10-649-857-45

Query Match 100.0%; Score 371; DB 15; Length 67;
 Best Local Similarity 100.0%; Pred. No. 6.2e-34;
 Matches 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGKCLRGAEELSLCFSFPPLPLHPTVAGRNGLGPBESLGVPPFLPHPGTTPRAPGFLLL 60
 Db 1 MGKCLRGAEELSLCFSFPPLPLHPTVAGRNGLGPBESLGVPPFLPHPGTTPRAPGFLLL 60

Qy 61 LPSFWAV 67
 Db 61 LPSFWAV 67

RESULT 3
 US-10-425-115-316330
 Sequence 316330, Application US/10425115
 Publication No. US20050107588A1
 GENERAL INFORMATION:
 APPLICANT: INCYTE GENOMICS, INC.

Query Match 22.5%; Score 83.5; DB 16; Length 98;
 Best Local Similarity 42.0%; Pred. No. 0.14;
 Matches 21; Conservative 5; Mismatches 15; Indels 9; Gaps 2;

Qy 16 SPPPLPLPLHPTVAGRNGLGP-----ESLGVPPFLPHPGTTPRAPGFL 58
 Db 51 SFPNKVPAFSRGLNSFPPLPKTPGPNPRGVPP--RNPGTSPRGPPIF 98

RESULT 4
 US-10-425-115-227490
 Sequence 227490, Application US/10425115
 Publication No. US2004014272A1
 GENERAL INFORMATION:
 APPLICANT: La Rossa, Thomas J.
 APPLICANT: Kovacic, David K.
 APPLICANT: Zhou, Yihua
 APPLICANT: Cao, Yongwei
 TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
 FILE REFERENCE: 38-21(53222)B
 CURRENT APPLICATION NUMBER: US/10/425,115
 NUMBER OF SEQ ID NOS: 369326
 SEQ ID NO 227490
 LENGTH: 139
 TYPE: PRT
 ORGANISM: zea mays
 FEATURE:
 NAME/KEY: unsure
 LOCATION: (1) .(139)
 OTHER INFORMATION: unsure at all Xaa locations
 OTHER INFORMATION: Clone ID: MRT4577_139067C.1.pep
 US-10-425-115-227490

Query Match 20.1%; Score 74.5; DB 16; Length 139;
 Best Local Similarity 37.9%; Pred. No. 2.1;
 Matches 22; Conservative 3; Mismatches 20; Indels 13; Gaps 3;

Qy 8 GAEGLSLESPFPPLPLHPTVAGRNGLGPESLGVPPFL--PHPGTTPRAPGFLLL 62
 Db 7 GEKEPFCF-FFP-----ENQKLGFPFGCLPDPFFCFVPPGKAKSSPGVFLPF 54

RESULT 5
 US-10-495-148-12
 Sequence 12, Application US/10495148
 Publication No. US20050107588A1
 GENERAL INFORMATION:
 APPLICANT: INCYTE GENOMICS, INC.

RESULT 6
 US-10-424-599-143004
 Sequence 143004, Application US/10424599
 Publication No. US2004031072a1
 GENERAL INFORMATION:
 / APPLICANT: La Rosa Thomas J
 / APPLICANT: Kovalic David K
 / APPLICANT: Zhou Yihua
 / APPLICANT: Cao Yongwei
 / TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
 / TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
 / FILE REFERENCE: 38-21(53221)B
 / CURRENT APPLICATION NUMBER: US/10/424,599
 / NUMBER OF SEQ ID NOS: 285684
 / SEQ ID NO 143004
 / LENGTH: 173
 / TYPE: PRT
 / ORGANISM: Glycine max
 / FEATURE:
 / OTHER INFORMATION: Clone ID: PAT_MRT3847_100146C.1.pep
 US-10-424-599-143004

Query Match 19.7%; Score 73; DB 15; Length 173;
 Best Local Similarity 40.0%; Pred. No. 4;
 Matches 20; Conservative 4; Mismatches 20; Indels 6; Gaps 2;

Qy 16 SPPPLPLPLHTPVAGRNLLGFPESLGVPPFLPHPGGTPRAPGLFLLLPSFW 65
 Db 110 SMAPVSRPVGTPLARRFSSFP--GGBP---PWGGDPHPVLDLPSFLW 153

RESULT 7
 US-10-437-963-175436
 Sequence 175436, Application US/10437963
 Publication No. US20040123343a1
 GENERAL INFORMATION:
 / APPLICANT: La Rosa, Thomas J.
 / APPLICANT: Kovalic, David K.
 / APPLICANT: Zhou, Yihua
 / APPLICANT: Cao, Yongwei
 / APPLICANT: Wu, Wei
 / APPLICANT: Boukharov, Andrey A.
 / APPLICANT: Barbazek, Brad
 / APPLICANT: Li, Ping
 / TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
 / TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
 / FILE REFERENCE: 38-21(53221)B
 / CURRENT APPLICATION NUMBER: US/10/437,963
 / NUMBER OF SEQ ID NOS: 204966
 / SEQ ID NO 175436
 / LENGTH: 104
 / TYPE: PRT
 / ORGANISM: Oryza sativa
 / FEATURE:
 / OTHER INFORMATION: Clone ID: PAT_MRT4530_73281C.1.pep
 US-10-437-963-175436

Query Match 19.3%; Score 71.5; DB 16; Length 104;
 Best Local Similarity 42.1%; Pred. No. 3 4;
 Matches 16; Conservative 6; Mismatches 15; Indels 1; Gaps 1;

Qy 30 GRNLGFPESLGVPPFLPHPGGTPRAPGLFLLF-SFWA 66
 Db 57 GRVKPFPGGGLPPEPPPGGAPPPEPSWKSPSFWA 94

RESULT 8
 10 ELSLCFSFPPLPLHTPVAGRNLLGFPESLGVPPFLPHPGGTPRAPGLFLL 60

Query Match 20.1%; Score 74.5; DB 17; Length 200;
 Best Local Similarity 41.2%; Pred. No. 3 2;
 Matches 21; Conservative 6; Mismatches 17; Indels 7; Gaps 3;

Qy ; NAME/KEY: midc_feature
 ; OTHER INFORMATION: Incyte ID No: 7762537CD1
 US-10-495-148-12

FEATURE: misc_feature
 NAME/KEY: misc_feature
 LOCATION: (1)..(672)
 OTHER INFORMATION: Xaa = any amino acid or nothing
 US-10-291-172-589

Query Match 19.1%; Score 71; DB 15; Length 672;
 Best Local Similarity 40.7%; Pred. No. 29;
 Matches 22; Conservative 1; Mismatches 17; Indels 14; Gaps 3;
 SEQ 19 PLILPLHTPVAGRNLGF--PESIG-----VPPFLPHPGGT---PRAAPGLF 58
 Db 589 PLQLPFHPPPLGLACGFLIPSSVGRDLGGFVPCFLGAQGAWFHIPRPTAF 642
 ; OTHER INFORMATION: Xaa = any amino acid or nothing
 US-10-221-278-588

RESULT 12
 US-10-221-278-587
 ; Sequence 587, Application US/10221278
 ; Publication No. US20040034208A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Hyseq, Inc.
 ; TITLE OF INVENTION: No. US20040034208A1 Nucleic Acids and Polypeptides
 ; FILE REFERENCE: 21272-045
 ; CURRENT APPLICATION NUMBER: US/10/221-278
 ; CURRENT FILING DATE: 2002-09-06
 ; PRIOR APPLICATION NUMBER: 09/693,267
 ; PRIOR FILING DATE: 2000-10-20
 ; PRIOR APPLICATION NUMBER: 09/665,363
 ; PRIOR FILING DATE: 2000-09-19
 ; PRIOR APPLICATION NUMBER: 09/616,847
 ; PRIOR FILING DATE: 2000-07-14
 ; PRIOR APPLICATION NUMBER: 09/596,193
 ; PRIOR FILING DATE: 2000-06-17
 ; PRIOR APPLICATION NUMBER: 09/574,454
 ; PRIOR FILING DATE: 2000-05-19
 ; PRIOR APPLICATION NUMBER: 09/519,705
 ; PRIOR FILING DATE: 2000-03-07
 ; NUMBER OF SEQ ID NOS: 752
 ; SEQ ID NO 587
 ; LENGTH: 672
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; FEATURE: misc_feature
 ; LOCATION: (1)..(672)
 ; OTHER INFORMATION: Xaa = any amino acid or nothing
 US-10-221-278-587

Query Match 19.1%; Score 71; DB 15; Length 672;
 Best Local Similarity 40.7%; Pred. No. 29;
 Matches 22; Conservative 1; Mismatches 17; Indels 14; Gaps 3;
 SEQ 19 PLILPLHTPVAGRNLGF--PESIG-----VPPFLPHPGGT---PRAAPGLF 58
 Db 589 PLQLPFHPPPLGLACGFLIPSSVGRDLGGFVPCFLGAQGAWFHIPRPTAF 642
 ; OTHER INFORMATION: Xaa = any amino acid or nothing
 US-10-221-278-588

RESULT 13
 US-10-221-278-588
 ; Sequence 588, Application US/10221278
 ; Publication No. US20040034208A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Hyseq, Inc.
 ; TITLE OF INVENTION: No. US20040034208A1 Nucleic Acids and Polypeptides
 ; FILE REFERENCE: 21272-045
 ; CURRENT APPLICATION NUMBER: US/10/221-278
 ; CURRENT FILING DATE: 2002-09-06
 ; PRIOR APPLICATION NUMBER: 09/693,267
 ; PRIOR FILING DATE: 2000-10-20
 ; PRIOR APPLICATION NUMBER: 09/665,363
 ; PRIOR FILING DATE: 2000-09-19
 ; PRIOR APPLICATION NUMBER: 09/616,847
 ; PRIOR FILING DATE: 2000-07-14
 ; PRIOR APPLICATION NUMBER: 09/596,193
 ; PRIOR FILING DATE: 2000-06-17
 ; PRIOR APPLICATION NUMBER: 09/574,454
 ; PRIOR FILING DATE: 2000-05-19
 ; PRIOR APPLICATION NUMBER: 09/519,705
 ; PRIOR FILING DATE: 2000-03-07
 ; NUMBER OF SEQ ID NOS: 752
 ; SEQ ID NO 589
 ; LENGTH: 672
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; FEATURE: misc_feature
 ; LOCATION: (1)..(672)
 ; OTHER INFORMATION: Xaa = any amino acid or nothing
 US-10-221-278-588

RESULT 14
 US-10-221-278-589
 ; Sequence 589, Application US/10221278
 ; Publication No. US20040034208A1
 ; GENERAL INFORMATION:
 ; APPLICANT: HYSEG, Inc.
 ; TITLE OF INVENTION: No. US20040034208A1 Nucleic Acids and Polypeptides
 ; FILE REFERENCE: 21272-045
 ; CURRENT FILING DATE: 2002-09-06
 ; PRIOR APPLICATION NUMBER: 09/633,267
 ; PRIOR FILING DATE: 2000-10-20
 ; PRIOR APPLICATION NUMBER: 09/665,363
 ; PRIOR FILING DATE: 2000-09-19
 ; PRIOR APPLICATION NUMBER: 09/616,847
 ; PRIOR FILING DATE: 2000-07-14
 ; PRIOR APPLICATION NUMBER: 09/596,193
 ; PRIOR FILING DATE: 2000-06-17
 ; PRIOR APPLICATION NUMBER: 09/574,454
 ; PRIOR FILING DATE: 2000-05-19
 ; PRIOR APPLICATION NUMBER: 09/519,705
 ; PRIOR FILING DATE: 2000-03-07
 ; NUMBER OF SEQ ID NOS: 752
 ; SEQ ID NO 589
 ; LENGTH: 672
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; FEATURE: misc_feature
 ; LOCATION: (1)..(672)
 ; OTHER INFORMATION: Xaa = any amino acid or nothing
 US-10-221-278-589

RESULT 15
 US-10-767-701-62790
 ; Sequence 62790, Application US/10767701
 ; Publication No. US2004017284A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Hyseq, Inc.
 ; TITLE OF INVENTION: No. US20040034208A1 Nucleic Acids and Polypeptides
 ; FILE REFERENCE: 21272-045
 ; CURRENT APPLICATION NUMBER: US/10/221-278
 ; CURRENT FILING DATE: 2002-09-06
 ; PRIOR APPLICATION NUMBER: 09/693,267
 ; PRIOR FILING DATE: 2000-10-20
 ; PRIOR APPLICATION NUMBER: 09/665,363
 ; PRIOR FILING DATE: 2000-09-19
 ; PRIOR APPLICATION NUMBER: 09/616,847
 ; PRIOR FILING DATE: 2000-07-14
 ; PRIOR APPLICATION NUMBER: 09/596,193
 ; PRIOR FILING DATE: 2000-06-17
 ; PRIOR APPLICATION NUMBER: 09/574,454
 ; PRIOR FILING DATE: 2000-05-19
 ; PRIOR APPLICATION NUMBER: 09/519,705
 ; PRIOR FILING DATE: 2000-03-07
 ; NUMBER OF SEQ ID NOS: 642
 ; SEQ ID NO 62790
 ; LENGTH: 672
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; FEATURE: misc_feature
 ; LOCATION: (1)..(672)
 ; OTHER INFORMATION: Xaa = any amino acid or nothing
 US-10-767-701-62790

Search completed: August 29, 2005, 20:48:13
Job time: 163 secs

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OM protein - protein search, using sw model

Run on: August 29, 2005, 20:45:34 ; Search time 168 Seconds (without alignments)

204.222 Million cell updates/sec

Title: US-10-649-857-45

Perfect score: 371

Sequence: 1 MGKOLCRGAELSLCSFPPL.....PGGTPRAGLFLFLFSFWAV 67

Scoring table: BLOSUM62

dapop dapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters:

1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_03:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	74.5	20.1	306	1 NG5_HUMAN	09946 homo sapien
2	72.5	19.7	200	2 Q6EZR36	06236 homo sapien
3	72.5	19.5	306	1 NG5_MOUSE	035449 mus musculu
4	71.5	19.3	297	2 Q17662	017662 caenorhabdi
5	71.5	19.3	1112	2 Q8GCT8	08978 mus musculu
6	70.5	19.0	216	2 Q9BEK5	09hek5 neurospora
7	70.5	19.0	313	2 Q976R7	0976r7 sulfolobus
8	70.0	18.9	142	2 P90815	p90815 caenorhabdi
9	69	18.6	123	2 Q9BBU5	09bbu5 homo sapien
10	69	18.6	241	2 Q9TIS4	09f184 arabidopsis
11	68.5	18.5	1802	2 Q17163	017163 brugia malae
12	68	18.3	85	2 Q8K4W4	08k4w4 mus musculu
13	68	18.3	123	2 Q8K4W5	08k4w5 mus musculu
14	67	18.1	481	2 Q071P5	007787 mycobacteri
15	67	18.1	481	2 Q071P5	07u1ps mycobacteri
16	66.5	17.9	145	2 Q94DT5	094dt5 oryza sativ
17	66.5	17.9	300	2 Q6mg82	06mg82 rattus norv
18	66.5	17.9	420	1 BD12_EBV	05225 Epstein-bar
19	66.5	17.9	420	2 Q777C4	0777c4 human herpe
20	66.5	17.9	703	2 Q8MM3	087mm3 vibrio para
21	66.5	17.9	718	2 Q6SK49	06sk49 arthrobacte
22	66	17.8	123	2 Q9WVJ1	09wv1 mus musculu
23	66	17.8	124	2 Q922F1	0922f1 rattus norv
24	66	17.8	381	2 Q67P01	06pall1 mus musculu
25	66	17.8	411	2 QEWJ00	06wj00 gallus gall
26	66	17.8	486	2 Q7RM4	07rm4 neurospora
27	66	17.8	517	2 Q73VN0	073vn0 mycobacteri
28	66	17.8	525	1 SR5VNO	P66845 mycobacteri
29	66	17.8	525	1 SR54_MYCB	P66844 mycobacteri
30	66	17.8	567	1 F2D7_CHICK	0573329 gallus gall
31	66	17.8	589	2 Q635094	0635094 rattus norv

ALIGNMENTS

RESULT 1		RESULT 1	
ID	NG5_HUMAN	ID	NG5_HUMAN
AC	Q9956 ; Q96DW3 ; Q96NO8 ;	AC	Q9956 ; Q96DW3 ; Q96NO8 ;
DT	28-FEB-2003 (Rel. 41, Created)	DT	28-FEB-2003 (Rel. 41, Last sequence update)
DT	05-JUL-2004 (Rel. 44, Last annotation update)	DT	05-JUL-2004 (Rel. 44, Last annotation update)
DB	Protein_N55.	DB	Protein_N55.
GN	Name=C6or31; Synonyms=RG5;	GN	Name=C6or31; Synonyms=RG5;
OS	Homo sapiens (Human)	OS	Homo sapiens (Human)
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX	NCBI_TaxID=9606;	OX	NCBI_TaxID=9606;
RN		RN	
RP	SEQUENCE FROM N.A. (ISOFORM 1).	RP	SEQUENCE FROM N.A. (ISOFORM 1).
RC		RC	
TISSUE=Cerebellum;		TISSUE=Cerebellum;	
PubMed=14702309; DOI=10.1038/ng1205;		PubMed=14702309; DOI=10.1038/ng1205;	
Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R., Wakanatsu A., Hayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S., Sekine M., Obayashi M., Nishi T., Nakamura Y., Yamamoto J.-I., Saito K., Kawai Y., Isono Y., Isono Y., Nakamura Y., Nagahari K., Murakami K., Yasuda T., Iwayanggi T., Wagatsuma M., Shiratori A., Sudo H., Hosoi T., Kaku Y., Kodaira H., Kondo H., Sugawara M., Takahashi M., Kanda K., Yokoji T., Furuya T., Kikkawa E., Omura Y., Abe K., Kamibara K., Katsuta N., Sato K., Tanikawa M., Yamazaki M., Niinomiya K., Ishibashi T., Yamashita H., Murakawa K., Fujimori K., Tanai H., Kimata M., HiraoKA M., Chiba Y., Ishida S., Ono Y., Takiguchi S., Watanabe S., Yosida M., Hotoda T., Kusano J., Kaehori K., Takahashi-Fujii A., Hara H., Tanase T.-O., Nomura Y., Togita Y., Konai F., Harr R., Takeuchi K., Arita M., Imose N., Musashino K., Yuuki H., Oshima A., Sasaki N., Aotsuka S., Yoshikawa Y., Matsunawa H., Ichihara T., Shiohata N., Sano S., Moriyama S., Moniyama H., Sato N., Takami S., Terashima Y., Suzuki O., Sanoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H., Hishigaki H., Watanabe T., Sugiyama A., Takanishi M., Kawakami B., Yamazaki M., Watanabe K., Kumagai A., Itikura S., Fukuzumi Y., Fujimori Y., Romiyama M., Tashiro H., Tanigami A., Fujisawa T., Ono T., Yamada K., Fujii Y., Ozaki K., Hirao M., Ohmori Y., Hikiji T., Kobatake N., Inagaki H., Ikeda Y., Okamoto S., Nakagawa S., Ono T., Nakagawa S., Sanoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H., Okitani R., Kawakami T., Noguchi S., Ichio T., Shigeta K., Senba T., Matsumura K., Nakajima Y., Mizuno T., Morinaga M., Saasaki M., Togashi T., Oyama M., Hata H., Watanabe M., Komatsu T., Mizushima-Sugano S., Sato T., Shirai Y., Nakagawa K., Okumura K., Nagase T., Nomura N., Kikuchi H., Masuho Y., Yamashita R., Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S., "Complete sequencing and characterization of 21,243 full-length human cDNAs.",	RT		

FT DOMAIN	41	49	Poly-His.	OC
FT DOMAIN	121	127	Poly-Pro.	OX
FT DOMAIN	128	131	Poly-Ala.	RN
FT DOMAIN	132	139	Poly-Pro.	RP
FT DOMAIN	203	206	Poly-Pro.	RX
SEQUENCE	306 AA;	31389 MW;	D88753;95737F386B CRC64;	SEQUENCE FROM N.A.
Query Match	19.5%	Score 72.5%; DB 1; Length 306;	"The Argonaute family: tentacles that reach into RNAi, developmental control, stem cell maintenance, and tumorigenesis.";	Medline=22301763; PubMed=12414724; DOI=10.1101/gad.1026102;
Best Local Similarity	41.2%; Pred. No. 9.7;	Indels 7; Gaps 3;	Genes Dev. 16:733-742(2002).	Carmel M.A., Xuan Z., Zhang M.Q., Hannon G.J.;
Matches 21; Conservative 6; Mismatches 17; Pred. No. 9.7;	Indels 7; Gaps 3;	RN [2]	control, stem cell maintenance, and tumorigenesis.";	
Qy 10 BLSLCFSTPFLPLPLPLPAGNLGPBISLGYPFPFLPHGGTPRABPLFL 60	SEQUENCE FROM N.A.	Adams M., Murai R.;	Genes Dev. 16:733-742(2002).	
Db 171 QLQPCPAYVP-VYVPGTPYAG--GTPGGPGVTSLLPBP--PQGFLALL 214	SEQUENCE FROM N.A.	Submitted (JUN-2002) to the EMBL/GenBank/DBDJ databases.	RN [2]	
RESULT 4				
017662	PRELIMINARY;	PRT;	297 AA.	RP
AC Q17662;				RA
DT 01-JAN-1998 (TRMBLrel. 05, Created)				RA
DT 01-JAN-1998 (TRMBLrel. 05, Last sequence update)				RA
DB Hypothetical protein C41G6.9.				RA
GN ORFNames=C41G6.9;				RA
OS Caenorhabditis elegans.				RA
OC Nematoda; Chromadorea; Rhabditida; Rhabditidae;				RA
RC Rhabditidae; Peioderinae; Caenorhabditis.				RA
RN [1]				RA
SEQUENCE FROM N.A.				RA
STRAIN=Bristol N2; PubMed=9851916;				RA
RX MEDLNB=99069613; PubMed=9851916;				RA
RA none;				RA
RT "Genome sequence of the nematode <i>C. elegans</i> : A platform for investigating biology.";				RA
RL Science 282:2012-2018 (1998).				RA
RP SEQUENCE FROM N.A.				RA
RN [2]				RA
RP SEQUENCE FROM N.A.				RA
RC STRAIN=Bristol N2;				RA
RA Cummings P.N.;				RA
RL Submitted (OCT-1996) to the EMBL/GenBank/DBDJ databases.				RA
DR CAB028341.1; -.				RA
PIR; T19888; T19888.				RA
DR WormBase; WBGenes00003381; C41G6.9.				RA
DR WormPep; C41G6.9; C815706.				RA
DR GO; GO:0016020; C:membrane; IEA.				RA
DR GO; GO:0004930; F:G-protein coupled receptor activity; IEA.				RA
DR InterPro; IPR001003; 7TM_chmreceptor2.				RA
DR Pfam; PF01604; 7TM_1.				RA
KW Hypothetical protein.				RA
SEQUENCE 297 AA; 33531 MW; 14F8C5873F534CA CRC64;				RA
Query Match	19.3%	Score 71.5%; DB 2; Length 297;	German Neurospora genome project;	SEQUENCE FROM N.A.
Best Local Similarity	51.2%; Pred. No. 12;	Indels 11; Gaps 3;	Submitted (NOV-2001) to the EMBL/GenBank/DBDJ databases.	RN [2]
Matches 22; Conservative 3; Mismatches 11; Indels 11; Gaps 3;			RP	RP
Qy 4 CL-CRGAEGLSLCFSFF--PFLPLPLPVAQRNLGPESLGPV 42	SEQUENCE FROM N.A.	Yakutkina U., Aign V., Hoheisel J., Brandt P., Hartmann B., Holland R., Schulte U., Mewes H.W., Maenhaut G.;	RP	RP
Db 61 CLHCVGAFDVFSSFAIPALNPIY--AGYFLGFSRVLGPV 100	SEQUENCE FROM N.A.	Submitted (DBC-2000) to the EMBL/GenBank/DBDJ databases.	RP	RP
RESULT 5				
QBGGT8	PRELIMINARY;	PRT;	1112 AA.	SEQUENCE FROM N.A.
AC QBGGT8;				Adams M., Murai R.;
DT 01-MAR-2003 (TRMBLrel. 23, Created)				Submitted (JUN-2002) to the EMBL/GenBank/DBDJ databases.
DT 01-MAR-2003 (TRMBLrel. 23, Last sequence update)				RN [2]
DT 01-JUN-2003 (TRMBLrel. 24, Last annotation update)				Adams M., Murai R.;
DB Argonaute 4 protein.				Submitted (JUN-2002) to the EMBL/GenBank/DBDJ databases.
GN Name=Pi2c1; Synonyms=Ago4;				RN [2]
OS Mus musculus (Mouse)				Adams M., Murai R.;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				Submitted (JUN-2002) to the EMBL/GenBank/DBDJ databases.
Query Match	19.0%	Score 70.5%; DB 2; Length 216;	Best Local Similarity	47.5%; Pred. No. 11;

Matches	19;	Conservative	3;	Mismatches	15;	Indels	3;	Gaps	3;		
Qy	21	LLPLHMP-WAGRNIGP-PESLQVPPPLPPIPGTTPA-PGL	57							[3]	SEQUENCE FROM N.A.
Db	68	MLPQNQPGGVPGLGPPIPAGVPPPPGMPPPPPGM	107	:						RC	STRAIN=Bristol N2;
RESULT 7											
Q976R7		PRELIMINARY;		PRT;		313 AA.				RN	SEQUENCE FROM N.A.
ID	Q976R7;									RP	RP
DT	01-DEC-2001	(TREMBLrel. 19,	Created)							RN	SEQUENCE FROM N.A.
DT	01-DEC-2001	(TREMBLrel. 19,	Last sequence update)							RP	SEQUENCE FROM N.A.
DT	01-JUN-2003	(TREMBLrel. 24,	Last annotation update)							RC	STRAIN=Bristol N2;
DB		Hypothetical protein	ST0123.							RA	Waterson R.
GN		OrderedLocusNames=	ST0123;							RL	Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
OS		Sulfolobus tokodaii.								RN	[4]
OC		Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;								RP	SEQUENCE FROM N.A.
OC		Sulfolobus.								RC	STRAIN=Bristol N2;
NCBI_TaxID	111955;									RA	Wilson R.;
RN	[1]									RA	Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
RP		SEQUENCE FROM N.A.								RL	Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
RC		STRAIN=21456156;								RN	[5]
RX		PubMed=11572479;								RP	SEQUENCE FROM N.A.
RA		Kawarabayasi Y., Hino Y., Horikawa H., Jin-no K., Takahashi M.,								RC	STRAIN=Bristol N2;
RA		Sekine M., Baba S.-I., Arka A., Kosugi H., Hosoyama A., Fukui S.,								RG	WormBase Consortium;
RA		Nagai Y., Nishijima K., Otsuka R., Nakazawa H., Takamiya M., Kato Y.,								RL	Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.
RA		Yoshizawa T., Tanaka T., Kudo Y., Yamazaki J., Kushida N., Oguchi A.,								DR	EMBL; US2002; AAB7732.1; -.
RA		Aoki K.-I., Masuda S., Yanagii M., Nishimura M., Yamagishi A.,								PIR	T29485; T29485.
RA		Oshima T., Kikuchi H.;								DR	WormBase; WBGS00017238; F08B4.7.
RT		"Complete genome sequence of an aerobic thermoacidophilic								DR	WormPep; F08B4.7; CE0923.2.
RT		Crenarchaeon, Sulfolobus tokodaii strain7.;"								DR	GO; 0005634; C-nucleus; IEA.
RI		DNA Res. 8:123-14 (2001).								DR	GO; 0008276; P-nucleic acid binding; IEA.
DR		EMBL; AP00981; BAB5079.1; -.								DR	GO; 0008276; P-zinc ion binding; IEA.
KW		Complete proteome; Hypothetical protein								DR	InterPro; IP000650; Znf-matrin.
SQ	SEQUENCE	313 AA;								PFam	PF06220; zf-U1; zf-U1.
Qy		PLLIPLHTPVAGRNLGPESLGLVPPFLPHGGTTPRAGL	57							DR	SMART; SM00451; zf-U1.
Db		92 PMMAP--RDPFGPGVGFPGAPGMPPFGPMPGMAGPPGM	128							DR	PROSITE; PSS0171; ZF-MATRIN; 1.
Query Match		18.9%								KW	Hypothetical protein.
Best Local Similarity		38.5%								SQ	SEQUENCE 142 AA; 15562 MW; 84ECB701A6BB9000 CRC64;
Matches	15;	Conservative	6;	Mismatches	6;	Indels	16;	Gaps	2;	DR	Query Match
Matches	18;	Conservative	11;	Mismatches	17;	Indels	5;	Gaps	2;	DR	Best Local Similarity
Matches	25;	Conservative	11;	Mismatches	16;	Indels	5;	Gaps	2;	DR	Best Local Similarity
Qy	16	SFPPLLLPLHTPVAGRNLGPESLGLVPPFLPHGGTTPRAGL	65							DR	Best Local Similarity
Db	137	NYWSLTIPAVILGVNIGNVTTATGVKPF--GLYQIPVLTINISMF	183							DR	Matches 15; Conservative 6; Mismatches 16; Indels 2; Gaps 1;
RESULT 8											
P908L5		PRELIMINARY;		PRT;		142 AA.				Q9BPU5	RESULT 9
ID	P908L5									ID	Q9BPU5
DT	01-MAY-1997	(TREMBLrel. 03,	Created)							AC	Q9BPU5
DT	01-MAY-1997	(TREMBLrel. 03,	Last sequence update)							DT	01-JUN-2001 (TREMBLrel. 17, Created)
DB	137	NYWSLTIPAVILGVNIGNVTTATGVKPF--GLYQIPVLTINISMF	183							DT	01-JUN-2003 (TREMBLrel. 17, Last sequence update)
DE		Hypothetical protein	F08B4.7.							DB	RT-1.
GN		ORFName=F08B4.7,	F08B4.7.							OS	Homosapiens (Human).
OS		Caenorhabditis elegans.								OC	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC		Caenorhabditis elegans.								OC	Mammalia; Eutheria; Primates; Catarrhini; Hominoidea.
NCBI_TaxID	6239;									NCBI_TaxID=9606;	Homo sapiens (Human).
RN	[1]									RN	SEQUENCE FROM N.A.
RP		SEQUENCE FROM N.A.								RC	TRIESTE=Brain;
RC		STRAIN=Bristol N2;								RA	PubMed=11159338; DOI=10.1093/hmg/10.3.201;
RX		PubMed=93069613;								RA	Wirth J., Back F., Hutterhofer A., Notthwang H.-G., Lich C., Gross S.,
RG		Wormbase Consortium;								RA	Menzel C., Schinzel A., Kioschis P., Tommerup N.T., Ropers H.-H.,
RT		"Genome sequence of the nematode <i>C. elegans</i> : a platform for								RA	Horsthemke B., Buiting K.;
RT		investigating biology." The <i>C. elegans</i> Sequencing Consortium. ";								RT	"A translocation cluster disrupts the newly defined 3' end
RL		Science 262:2012-2018 (1998).								RT	RT of the SNURP-SNRP transcription unit on chromosome 15. ";
RN	[2]									RL	Hum. Mol. Genet. 10:201-210 (2001).
RP		SEQUENCE FROM N.A.								DR	DR; AF11953; AAK18178.1; -.
RC		STRAIN=Bristol N2;								RA	SEQUENCENCB 123 AA; 1233 MW; DBB7AF48D20CFDC CRC64;
RX		Stellye L., Gattung S.;								RA	"The sequence of <i>C. elegans</i> cosmid F08B4.7;
RT		Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.								RL	Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.

Matches	16; .Conservative	4;	Mismatches	19;	Indels	4;	GapB	1;	SQ	SEQUENCE	1802 AA;	172402 MW;	595F16554CBB2D24 CRC64;
Qy	27 PVAGRNLGFPESTGVPPFLPHPGCTPRAGL---FNUFLSEFW	65								Query Match	18.5%;	Score 68.5;	DB 2;
Db	56 PPNGPPCIGLPPARPGTPIGMPPGMRPPGIRGEAFLALVCW	98								Best Local Similarity	51.2%;	Pred. No. 1.5e-02;	
RESULT 10													
Q9F1S4	PRELIMINARY;		PRT;	241 AA.						Matches	22;	Conservative	0; Mismatches 16; Indels 5; Gaps 3;
AC	Q9F1S4									Q8K4W4		PRELIMINARY;	
DT	01-MAR-2001	(TREMBLrel. 16, Created)								AC	Q8K4W4;		
DT	01-MAR-2001	(TREMBLrel. 16, Last sequence update)								DT	01-OCT-2002	(TREMBLrel. 22, Created)	
DB	Arabidopsis thaliana	genomic DNA, chromosome 5, P1 clone:MTG10.								DT	01-OCT-2002	(TREMBLrel. 22, Last sequence update)	
OS	Arabidopsis thaliana	(Mouse-ear cress).								DT	01-MAR-2004	(TREMBLrel. 26, Last annotation update)	
OC	Bukaryota; Viridiplantae; Streptopterygia; Embryophyta; Tracheophyta;									DB	Calmodulin-dependent protein kinase II beta 3 isoform	insert	
OC	Spermatophyta; Magnoliophyta; eudicots; rosids;									DB	(Fragment).		
OC	eudicots II; Brassicales; Brassicaceae; Arabidopsis.									GN	Name=Cam2b;		
OX	NCBI_TaxID=3702;									OS	Mus musculus	(Mouse).	
RN	SEQUENCE FROM N.A.									OC	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
RX	MEDLINE=99087489; PubMed=9872454;									OC	Mammalia; Eutheria; Rodentia; Muridae; Murinae; Mus.		
RA	Nakamura Y., Sato S., Asanizu B., Kaneko T., Kotani H., Miyajima N.,									OX			
RA	Tabata S.;									[1]			
RT	"Structural analysis of Arabidopsis thaliana chromosome 5, VII. Sequence features of the regions of 1,013,767 bp covered by sixteen physically assigned P1 and TAC clones."									RN	SEQUENCE FROM N.A.		
RT	Sequence features of the regions of 1,013,767 bp covered by sixteen physically assigned P1 and TAC clones."									RC	STRAIN=BALB/c;		
RL	5,297-308 (1998).									RX	PubMed=12110572; DOI=10.1093/embj/cdf360;		
DR	DNA Res.									RA	Bayer K.U., De Koninck P., Schulman H.;		
EMBL; AB016880; BAB10176.1; "										RT	"Alternative splicing modulates the frequency-dependent response of CAMKII to Ca2+ oscillations."		
SEQUENCE	241 AA;	26439 MW;	F8920D05D4E6DF6F	CRC64;						RL	EMBO J. 21:3590-3597(2002).		
Query Match	18.6%;	Score 69;	DB 2;	Length 241;						RN	[2]		
Best Local Similarity	43.2%;	Pred. No. 18;								RP	SEQUENCE FROM N.A.		
Matches	16; .Conservative	6;	Mismatches	11;	Indels	4;	GapB	1;		RC	STRAIN=BALB/c;		
Qy	9 ATISLCLFSPFPULLPLHPTPVAGRNLGFPESTGVPPFL	45								RA	Bayer K.-U.;		
Db	97 SEASVCPNATVYIYPSISQTQTKPLGP---LPPFL	129								RA	Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.		
RESIDUE 11										RA	EMBL; AF416337; AAC77845.1; JOINED.		
Q17163	PRELIMINARY;		PRT;	1802 AA.						KW	Cam2b activity		
ID	Q17163;									DR	DR; GO; GO:0016301; F:kinase activity; IEA.		
AC	Q17163;									DR	GO; GO:0016301; F:kinase activity; IEA.		
DT	01-NOV-1996	(TREMBLrel. 01, Created)								DR	GO; GO:0016301; F:kinase activity; IEA.		
DT	01-NOV-1996	(TREMBLrel. 01, Last sequence update)								FT	NON-TER	1	1
DT	01-OCT-1993	(TREMBLrel. 25, Last annotation update)								FT	NON-TER	85	85 AA;
DB	A2 (IV) basement membrane collagen.									FT	SEQUENCE	85 AA;	BFLAB9082AOE5316 CRC64;
OS	Brugia malayi (Filarial nematode worm).									FT			
OC	Bukaryota; Metazoa; Nematoda; Chromodorea; spirurida; Filarioidea;									FT			
ON	Onchocercidae; Brugia.									FT			
RN	NCBI_TaxID=6279;									FT			
RC	SEQUENCE FROM N.A.									FT			
RX	CAULAGI V.R., Rajan T.V.									FT			
RT	"The structural organization of an alpha 2 (type IV) basement membrane collagen gene from the filarial nematode <i>Brugia malayi</i> ."									FT			
RT	"The structural organization of an alpha 2 (type IV) basement membrane collagen gene from the filarial nematode <i>Brugia malayi</i> ."									FT			
RL	Mol. Biochem. Parasitol. 70:227-229(1995).									FT			
EMBL; U07224; AAC46611.1;	-.									FT			
DR	HSSP; P08572; 1111.									FT			
DR	GO; GO:0005581; C:collagen; IEA.									FT			
DR	GO; GO:005737; C:cytoskeleton; IEA.									FT			
DR	GO; GO:0005201; F:extracellular matrix structural constituent; IEA.									FT			
DR	GO; GO:000817; P:phosphate transport; IEA.									FT			
DR	InterPro; IPR00810; Collagen.									FT			
DR	InterPro; IPR001442; Procollagen4 C.									FT			
DR	Pfam; PF01413; C4_2.									FT			
DR	SMART; SM00111; C4_2.									FT			
DR	Collagen.									FT			

Q1	SEQUENCE FROM N.A.	SEQUENCE	481 AA;	50764 MW;	726E8265DCCA6A29 CRC64;
RP	SEQUENCE FROM N.A.				
RC	STRAIN=BALB/c;				
RX	PubMed=12.110572; DOI=10.1093/embj/cdf3360;				
RA	Bayer K.U.; De Koninck P.; Schulman H.;				
RT	"Alternative splicing modules the frequency-dependent response of CAMKII to Ca ²⁺ oscillations.";				
RT	EMBO J. 21:3590-3597(2002).				
[2]					
RN	SEQUENCE FROM N.A.				
RP	STRAIN=BALB/c;				
RA	Bayer K.U.;				
RA	Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.				
DR	EMBL; AP416337; AAW7844.1;				
DR	EMBL; AP416336; AAW7844.1; JOINED.				
GO	GO:0016301; P:Kinase activity; IEA.				
KW	Kinase.				
FT	NON_TER 1				
FT	NON_TER 123 AA; 123 AA; 12304 MW; C45A4D20531B9347 CRC64;				
SQ	SEQUENCE 123 AA; 12304 MW; C45A4D20531B9347 CRC64;				
Qy	4 CLCRGAELSLCSFSEPPFLPLHPT-----VAGRNLGFPESLGVPPFLPHPGCTPRA 54				
Db	68 CLSPG-----LLGPLTPSPRISDILNSVRSGTTDEAEGLPPVGPPCPSPPTL 116				
Qy	55 PG 56				
Db	117 PG 118				
SQ	SEQUENCE 21; Conservative 33.9%; Pred. No. 12; Indels 18; Gaps 2;				
Matches 21;	Best Local Similarity 33.9%; Pred. No. 12;				
Matches 21;	Score 68; DB 2; Length 123;				
Qy	007787 PRELIMINARY; PRT; 481 AA.				
AC	007787				
DT	01-JUL-1997 (T-EMBLrel. 04, Created)				
DT	01-JUL-1997 (T-EMBLrel. 04, Last sequence update)				
DT	01-OCT-2003 (T-EMBLrel. 25, Last annotation update)				
DB	NCBI-FAMILY PROTEIN MC22C.				
GN	Name=mc22C; OrderedLocusNames=Rv0591;				
OS	Mycobacterium tuberculosis.				
OC	Corynebacterineae; Actinobacteridae; Actinomycetales;				
OC	Corynebacterineae; Mycobacteriaceae; Mycobacterium.				
OX	NCBI_TaxID=1773;				
RN	SEQUENCE FROM N.A.				
RC	STRAIN=H37Rv;				
RX	PubMed=9634210; DOI=10.1038/31159;				
RA	Cole S.T., Btrosch R., Parthill J., Garnier T., Churcher C.M., Harris D.E., Barry C.E. III, Barry C.E. III,				
RA	Tekai F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R.M., Devin K., Feltwell T., Gentles S., Hamlin N., Holroyd S., Hornsby T., Jagels K., Krogh A., McLean J., Moulie S., Murphy L.D., Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squires R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;				
RT	"Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence."				
RT	Nature 393:517-544 (1998).				
RL	PIR; B70908; B70908.				
DR	DR; BX842574; CAB08961.1; -.				
DR	TubercList; Rv0591; -.				
DR	GO; GO:0009405; P:pathogenesis; IEA.				
DR	InterPro; IPR005693; Mce.				
DR	InterPro; IPR005336; Mce1C.				
DR	InterPro; IPR001339; Mce_rel.				
DR	PF02470; Mce; 1.				
DR	TIGRFAMS; TIGR00996; Mtu_fam_mce; 1.				
DR	Complete proteome.				
KW					

Result No.	Score	query Match	Length	DB ID	Description
1	64.5	17.4	426	4	US-09-889-039A-11995 Sequence 11995, A
2	63.5	17.1	751	4	US-09-543-68A-4181 Sequence 4181, AP
3	63.5	17.1	847	4	US-09-949-016-6222 Sequence 6222, AP
4	63.5	17.1	885	4	US-09-949-016-7789 Sequence 7789, AP
5	63	17.0	265	1	US-08-155-17B-41 Sequence 41, APP1
6	63	17.0	265	2	US-08-135-99B-41 Sequence 34, APP1
7	63	17.0	277	4	US-09-331-887-34 Sequence 26182, A
8	63	17.0	582	4	US-09-232-99A-26182 Sequence 19452, A
9	62.5	16.8	422	4	US-09-352-99A-10452 Sequence 10554, A
10	62	16.7	248	4	US-09-949-016-10554 Sequence 96, APP1
11	62	16.7	249	4	US-09-947-254-96 Sequence 41, APP1
12	62	16.7	265	2	US-08-135-99B-41 Sequence 34, APP1
13	61.5	16.6	277	4	US-09-331-887-34 Sequence 26182, A
14	61.5	16.6	582	4	US-09-232-99A-26182 Sequence 18762, A
15	61.5	16.6	305	4	US-09-232-99A-10452 Sequence 37797, A
16	61.5	16.6	426	4	US-09-270-767-53014 Sequence 53014, A
17	61.5	16.6	664	4	US-09-232-99A-29360 Sequence 29360, A
18	61	16.6	515	4	US-09-232-99A-28127 Sequence 83127, A
19	61.5	16.6	169	4	US-09-489-039A-8371 Sequence 8371, AP
20	61.5	16.6	305	4	US-09-232-99A-18176 Sequence 18762, A
21	61.5	16.6	426	4	US-09-270-767-37797 Sequence 37797, A
22	61	16.4	426	4	US-09-270-767-53014 Sequence 53014, A
23	61	16.4	664	4	US-09-232-99A-29360 Sequence 29360, A
24	61	16.4	240	4	US-09-819-989-2 Sequence 2, APP1
25	61	16.4	811	4	US-10-273-992-2 Sequence 2, APP1
26	61	16.4	1572	4	US-09-302-540-12652 Sequence 12652, A
27	60.5	16.3	240	4	US-09-538-092-930 Sequence 930, APP

Best Local Similarity 37.7%; Pred. No. 24;
Matches 23; Conservative 3; Mismatches 18; Indels 17; Gaps 4;
Score 63.5; DB 4; Length 885;
Query Match 17.1%; Score 63.5; DB 4; Length 885;
Best Local Similarity 31.9%; Pred. No. 29;
Matches 22; Conservative 6; Mismatches 20; Indels 21; Gaps 3;
Query 13 LCRSF-----FPLPLHPTVAGRNGLGFP-----SLGVPP-----FPLPHPGGT 51
Db 734 ICPFLKTPDSPTPAPLIDLGIPVQRSAKSPRREERPRGGTVSPPPOTSRSAPGTP 793
Qy 52 PRAPGLFL 60
Db 794 PRSPPLGLI 802

RESULT 3
US-09-949-016-6222
1 Sequence 6222, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 6222
; LENGTH: 847
; TYPE: PRT
; ORGANISM: Human
; US-09-949-016-6222

Query Match 17.1%; Score 63.5; DB 4; Length 847;
Best Local Similarity 31.9%; Pred. No. 28; Mismatches 20; Indels 21; Gaps 3;
Query 13 LCRSF-----FPLPLHPTVAGRNGLGFP-----SLGVPP-----FPLPHPGGT 51
Db 696 ICPFLKTPDSPTPAPLIDLGIPVQRSAKSPRREERPRGGTVSPPPOTSRSAPGTP 755
Qy 52 PRAPGLFL 60
Db 756 PRSPPLGLI 764

RESULT 4
US-09-949-016-7789
; Sequence 7789, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 7789
; LENGTH: 885
; TYPE: PRT
; ORGANISM: Human

Query Match 17.0%; Score 63.; DB 1; Length 265;
Best Local Similarity 36.8%; Pred. No. 8.5;
Matches 21; Conservative 9; Mismatches 15; Indels 12; Gaps 4;
Query 7 RGAESLICCSFFPL-----LPLHPTVAGRNGLGFP-----SLGVPP-----FPLPHPGGT 54
Db 162 QGAALSP-TTYPKTPKILPMATVYQGNENVPMLEPP-LPPTIAADPVGSVVA 215

RESULT 6
US-08-435-998-41

```

Sequence 41, Application US/08435998
GENERAL INFORMATION:
APPLICANT: Anderson, Carl W.
APPLICANT: Mangel, Walter F.
TITLE OF INVENTION: Co-Factor Activated Recombinant
TITLE OF INVENTION: Adenovirus Proteases (As Amended)
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Millenia Drive
CITY: Lexington
STATE: Massachusetts
COUNTRY: USA
ZIP: 02473

COMPUTER READABLE FORM:
COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/435,998
FILING DATE: 05-MAY-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/155,171
FILING DATE: 19-NOV-1993
APPLICATION NUMBER: US 07/851,217
FILING DATE: 13-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/545,585
FILING DATE: 29-JUN-1990
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: BNL91-01A2, AUI93-22
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 861-6240
TELEFAX: (617) 861-9540
INFORMATION FOR SEQ ID NO: 41:
SEQUENCE CHARACTERISTICS:
LENGTH: 265 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-435-998-41

Query Match
Best Local Similarity 17.0%; Score 63; DB 2; Length 265;
Matches 21; Conservative 9; Mismatches 15; Indels 12; Gaps 4;
Qy 7 RGAELSLCSFPLP--LPLIHTPVAGRNLGPFPESLGVPPLPHP---GGTPRA 54
Db 162 QGRALSP--TTRYPMTKPLMPATRYKNEVNPMTLELPP-LPBPPTADPGSVPVA 215

RESULT 7
US-09-431-887-34
Sequence 34, Application US/09431887
GENERAL INFORMATION:
APPLICANT: D-Gen Limited
TITLE OF INVENTION: BIOLOGICAL MATERIALS AND METHODS USEFUL IN THE
DISEASES OF PRION DISEASE
FILE REFERENCE: ICOT/P21952
CURRENT APPLICATION NUMBER: US/09/431,887
CURRENT FILING DATE: 1999-11-02
PRIOR APPLICATION NUMBER: GB 9824091-4
PRIOR FILING DATE: 1999-11-04
NUMBER OF SEQ ID NOS: 37
SEQ ID NO 34
LENGTH: 277

Query Match
Best Local Similarity 17.0%; Score 63; DB 4; Length 277;
Matches 14; Conservative 3; Mismatches 15; Indels 2; Gaps 1;
Qy 25 HTTPVAGRNLGPFPESLGVPPLPH-PGCTPRA 56
Db 58 HNPGPHPNPGYPNNPGYPNGPYPNGPYPONPG 91

RESULT 8
US-09-252-991A-26182
Query Match
Best Local Similarity 17.0%; Score 63; DB 4; Length 582;
Matches 14; Conservative 4; Mismatches 15; Indels 8; Gaps 1;
Qy 19 PILLPLIHTPVAGRNLG-----PESLGVPPLPHPGGT 51
Db 117 PDLVLRHQPAGCHGAGTAPAGQHRRPDRPAQPLVYAPGQT 157

RESULT 9
US-09-252-991A-19452
Query Match
Best Local Similarity 17.0%; Score 63; DB 4; Length 582;
Matches 14; Conservative 4; Mismatches 15; Indels 8; Gaps 1;
Qy 19 PILLPLIHTPVAGRNLG-----PESLGVPPLPHPGGT 51
Db 117 PDLVLRHQPAGCHGAGTAPAGQHRRPDRPAQPLVYAPGQT 157

RESULT 10
US-09-252-991A-19452
Query Match
Best Local Similarity 34.1%; Score 63; DB 4; Length 582;
Matches 14; Conservative 4; Mismatches 15; Indels 8; Gaps 1;
Qy 19 PILLPLIHTPVAGRNLG-----PESLGVPPLPHPGGT 51
Db 117 PDLVLRHQPAGCHGAGTAPAGQHRRPDRPAQPLVYAPGQT 157

RESULT 11
US-09-252-991A-19452
Query Match
Best Local Similarity 34.1%; Score 63; DB 4; Length 582;
Matches 14; Conservative 4; Mismatches 15; Indels 8; Gaps 1;
Qy 19 PILLPLIHTPVAGRNLG-----PESLGVPPLPHPGGT 51
Db 117 PDLVLRHQPAGCHGAGTAPAGQHRRPDRPAQPLVYAPGQT 157

RESULT 12
US-09-252-991A-19452
Query Match
Best Local Similarity 34.1%; Score 63; DB 4; Length 582;
Matches 14; Conservative 4; Mismatches 15; Indels 8; Gaps 1;
Qy 19 PILLPLIHTPVAGRNLG-----PESLGVPPLPHPGGT 51
Db 117 PDLVLRHQPAGCHGAGTAPAGQHRRPDRPAQPLVYAPGQT 157

RESULT 13
US-09-252-991A-19452
Query Match
Best Local Similarity 34.1%; Score 63; DB 4; Length 582;
Matches 14; Conservative 4; Mismatches 15; Indels 8; Gaps 1;
Qy 19 PILLPLIHTPVAGRNLG-----PESLGVPPLPHPGGT 51
Db 117 PDLVLRHQPAGCHGAGTAPAGQHRRPDRPAQPLVYAPGQT 157

RESULT 14
US-09-252-991A-19452
Query Match
Best Local Similarity 34.1%; Score 63; DB 4; Length 582;
Matches 14; Conservative 4; Mismatches 15; Indels 8; Gaps 1;
Qy 19 PILLPLIHTPVAGRNLG-----PESLGVPPLPHPGGT 51
Db 117 PDLVLRHQPAGCHGAGTAPAGQHRRPDRPAQPLVYAPGQT 157

```

RESULT 10
 US-03-949-016-10554
 Sequence 10554, Application US/09949016
 Patent No. 6812339
 GENERAL INFORMATION:
 APPLICANT: VENTER, J. Craig et al.
 TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
 CURRENT APPLICATION NUMBER: C1001307
 CURRENT FILING DATE: 2000-04-14
 PRIOR APPLICATION NUMBER: 60/241,755
 PRIOR FILING DATE: 2000-10-20
 PRIOR APPLICATION NUMBER: 60/227,768
 PRIOR FILING DATE: 2000-10-03
 PRIOR APPLICATION NUMBER: 60/231,498
 PRIOR FILING DATE: 2000-09-08
 NUMBER OF SEQ ID NOS: 207012
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO 10554
 LENGTH: 248
 TYPE: PRT
 ORGANISM: Human
 US-09-949-016-10554

Query Match 16.7%; Score 62; DB 4; Length 248;
 Best Local Similarity 40.0%; Pred. No. 10;
 Matches 14; Conservative 3; Mismatches 18; Indels 0; Gaps 0;

Qy 27 PVAQRNLGFPESSLGVPPPELPHPGTTPRAGNLFLL 61
 Db 214 PPMGPMGIPPGRGTIPGMPPGMRPPGMRGILL 248

RESULT 11
 US-09-917-254-96
 Sequence 96, Application US/09917254
 Patent No. 6703204
 GENERAL INFORMATION:
 APPLICANT: Mutter, George
 APPLICANT: Baak, Jan
 TITLE OF INVENTION: Prognostic Classification of Breast Cancer
 FILE REFERENCE: B0801/27224 (JPR)
 CURRENT APPLICATION NUMBER: US/09/917,254
 CURRENT FILING DATE: 2001-07-27
 PRIOR APPLICATION NUMBER: US 60/222,093
 PRIOR FILING DATE: 2000-07-28
 NUMBER OF SEQ ID NOS: 102
 SOFTWARE: PatentIn version 3.0
 SEQ ID NO 96
 LENGTH: 249
 TYPE: PRT
 ORGANISM: Homo Sapiens
 US-09-917-254-96

Query Match 16.7%; Score 62; DB 4; Length 249;
 Best Local Similarity 40.0%; Pred. No. 10;
 Matches 14; Conservative 3; Mismatches 18; Indels 0; Gaps 0;

Qy 27 PVAQRNLGFPESSLGVPPPELPHPGTTPRAGNLFLL 61
 Db 215 PPMGPMGIPPGRGTIPGMPPGMRPPGMRGILL 249

RESULT 12
 US-09-991A-28127
 Sequence 28127, Application US/09252931A
 Patent No. 6551795
 GENERAL INFORMATION:
 APPLICANT: Marc J. Rubenfield et al.
 TITLE OF INVENTION: NUCLEIC ACID SEQUENCES RELATING TO PSEUDOMONAS

RESULT 13
 US-09-489-039A-8371
 Sequence 8371, Application US/09489039A
 Patent No. 6610836
 GENERAL INFORMATION:
 APPLICANT: Gary Breton et. al.
 TITLE OF INVENTION: NUCLEAR ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
 CURRENT APPLICATION NUMBER: US/09/489,039A
 CURRENT FILING DATE: 2000-01-27
 PRIOR APPLICATION NUMBER: US 60/117,747
 PRIOR FILING DATE: 1999-01-29
 NUMBER OF SEQ ID NOS: 14342
 SEQ ID NO 8371
 LENGTH: 169
 TYPE: PRT
 ORGANISM: Klebsiella pneumoniae
 FEATURE:
 NAME/KEY: UNSURE
 LOCATION: (10), (11), (12), (13), (14), (15), (16), (17), (18), (19), (20), (21), (22), (23), (24), (25), (26), (27), (28), (29), (30), (31), (32), (33), (34), (35)
 LOCATION: (23), (24), (25), (26), (27), (28), (29), (30), (31), (32), (33), (34), (35)
 OTHER INFORMATION: Identity of amino acid at the above locations are unknown.
 US-09-489-039A-8371

Query Match 16.6%; Score 61.5; DB 4; Length 169;
 Best Local Similarity 40.0%; Pred. No. 7,7;
 Matches 18; Conservative 2; Mismatches 22; Indels 3; Gaps 1;

Qy 17 FFPPLPLHPTPVAGRNLGFPESSLGVPPPELPHPGTTPRAGNLFLL 61
 Db 100 FSPSSLPPFSPPPSLFSPPSS--PPUULLSPSPSPLLLIL 141

RESULT 14
 US-09-252-991A-18762
 Sequence 18762, Application US/09252991A
 Patent No. 6551795
 GENERAL INFORMATION:
 APPLICANT: Marc J. Rubenfield et al.
 TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
 FILE REFERENCES: 10/196.136
 CURRENT FILING DATE: 1999-02-18
 PRIOR APPLICATION NUMBER: US 60/074,788
 PRIOR FILING DATE: 1998-02-18
 PRIOR APPLICATION NUMBER: US 60/094,190
 PRIOR FILING DATE: 1998-07-27

Search completed: August 29, 2005, 20:37:03

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GenCore version 5.1.6

Run on: August 29, 2005, 20:37:09 ; Search time 39 Seconds
(without alignments)

165.295 Million cell updates/sec

Title: US-10-649-857-45

Perfect score: 371

Sequence: 1 MGKCLQRGABISLCFSFFPL..... PEGTTPRAGLFLLPSFWAV 67

Scoring table: BIOSTM62

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416
ALIGNMENTS

Minimum DB seq length: 0
Maximum DB seq length: 200000000
RESULT 1
T09067
extensin-like protein NG5 - mouse
C:Species: *Mus musculus* (house mouse)

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79,*
 1: pir1:*

A;Description: Sequence of the mouse major histocompatibility locus class III
 A;Reference number: Z16543
 A;Accession: T09067
 A;Status: preliminary; translated from GB/EMBL/DDBJ

4: p1r4: * A;Molecule type: DNA
A;Residues: 1-106 <ROW>
A;Cross-references: UNIPROT:O35449; EMBL:AF030001; NID:92564945; PID:g2564955
C;Genetics:
A;Gene: NGS
A;Gene ID: 17
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARTES A/Infrastrukturposition: 7/1 186/3. 248/3

THE JOURNAL OF CLIMATE

Result No.	Score	Query	Match	Length	ID	Description			
						Extensin-like protein	hypothetical protein	hypothetical protein	macrolide-lincosamides
1	72.5	19.5	306	2	T09067				
2	71.5	19.3	297	2	T19888				
3	70	18.9	142	2	T29485				
4	69.5	18.7	327	2	JCS319				

22	63	17.0	265	1	B45393	C;Genetics:		Score 71.5;	Length 297;
23	63	17.0	273	2	A46280	A;Gene: C31G6.9			
24	62.5	16.8	295	2	T28078	A;Map Position: 5			
25	62	16.7	214	2	B34503	A;Introns: 114; 125/2; 168/3; 240/1			
26	62	16.7	231	2	I53659	C;Superfamily: Caenorhabditis hypothetical protein C49G7.2			
27	61.5	16.6	197	2	H86979				
28	61.5	16.6	211	2	S615129	Query Match 19.34;			
29	61.5	16.6	564	2	AG2823	Best Local Similarity 51.24;			
						Best Predictor No. 1.4;			

Matches 22; Conservative 3; Mismatches 11; Indels 7; Gaps 3; R; Cole, S.T.; Brooch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. C; Species: *Caenorhabditis elegans* Q; Date: 15-Oct-1999 #text_change 09-Jul-2004 C; Accession: T29485 C; Status: preliminary; translated from GB/EMBL/DBJ R; Stellies, L.; Gartung, S. Submitted to the EMBL Data Library, March 1996 A; Description: The sequence of *C. elegans* cosmid F08B4. A; Reference number: Z20625 A; Accession: T29485 A; Status: preliminary; translated from GB/EMBL/DBJ A; Molecule type: DNA A; Residues: 1-142 <STR> A; Cross-references: UNIPROT:P09815; EMBL:U52002; PIDN:AAB37732.1; GSFPDB:GN00022; CESP:PG C; Experimental source: strain Bristol N2; clone F08B4 A; Gene: CESP:F08B4.7 A; Map Position: 4 A; Introns: 3/9/3; 61/3; 111/3 C; Superfamily: proline-rich protein

Query Match 18.9%; Score 70; DB 2; Length 142; Best Local Similarity 38.5%; Pred. No. 1; Matches 15; Conservative 6; Mismatches 16; Indels 2; Gaps 1; R; Cole, S.T.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. C; Species: *Streptomyces fradiae* Q; Date: 01-May-1997 #sequence_revision 18-Jul-1997 #text_change 09-Jul-2004 C; Accession: JCS319 R; Gandeche, A.R.; Cundliffe, B. Gene 180, 173-176, 1996 A; Article: Molecular analysis of tlrD, an MLS resistance determinant from the tylosin producer *Streptomyces fradiae* A; Reference number: JCS319; MUID:9712823; PMID:8973363 A; Molecule type: DNA A; Residues: 1-27 <STR> A; Cross-references: UNIPROT:P97178; EMBL:X97721; PIDN:CAA66307.1; PID:9178 C; Comment: This protein monomethylates residue A-2058 in 23S rRNA generating N6-methylated C; Genetics: A; Gene: tlrD C; Superfamily: rRNA (adenine-N6-) -methyltransferase

Query Match 18.7%; Score 69.5%; DB 2; Length 327; Best Local Similarity 45.0%; Pred. No. 2, 6; Matches 18; Conservative 2; Mismatches 17; Indels 3; Gaps 1; R; Cole, S.T.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. C; Species: *Mycobacterium tuberculosis* Q; Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004 C; Accession: B70908 A; Status: preliminary; nucleic acid sequence not shown; translation not shown A; Molecule type: DNA A; Residues: 1-525 <COL> A; Cross-references: UNIPROT:Q10963; GB:Z74697; PIDN:CAA98978. R; Cole, S.T.; Brooch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. C; Species: *Mycobacterium tuberculosis* Q; Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004 C; Accession: B70908 A; Status: preliminary; nucleic acid sequence not shown; translation not shown A; Molecule type: DNA A; Residues: 1-525 <COL> A; Cross-references: UNIPROT:Q10963; GB:Z74697; PIDN:CAA98978.

RESULT 3 T29485 hypothetical protein F08B4.7 - *Caenorhabditis elegans* C; Species: *Caenorhabditis elegans* Q; Date: 15-Oct-1999 #text_change 09-Jul-2004 C; Accession: T29485 C; Status: preliminary; translated from GB/EMBL/DBJ R; Stellies, L.; Gartung, S. Submitted to the EMBL Data Library, March 1996 A; Description: The sequence of *C. elegans* cosmid F08B4. A; Reference number: Z20625 A; Accession: T29485 A; Status: preliminary; translated from GB/EMBL/DBJ A; Molecule type: DNA A; Residues: 1-142 <STR> A; Cross-references: UNIPROT:P09815; EMBL:U52002; PIDN:AAB37732.1; GSFPDB:GN00022; CESP:PG C; Genetics: A; Gene: CESP:F08B4.7 A; Map Position: 4 A; Introns: 3/9/3; 61/3; 111/3 C; Superfamily: proline-rich protein

Query Match 18.1%; Score 67; DB 2; Length 481; Best Local Similarity 40.5%; Pred. No. 7, 3; Matches 15; Conservative 3; Mismatches 13; Indels 6; Gaps 1; R; Cole, S.T.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. C; Species: *Streptomyces fradiae* Q; Date: 01-May-1997 #sequence_revision 18-Jul-1997 #text_change 09-Jul-2004 C; Accession: JCS319 R; Gandeche, A.R.; Cundliffe, B. Gene 180, 173-176, 1996 A; Article: Molecular analysis of tlrD, an MLS resistance determinant from the tylosin producer *Streptomyces fradiae* A; Reference number: JCS319; MUID:9712823; PMID:8973363 A; Molecule type: DNA A; Residues: 1-27 <STR> A; Cross-references: UNIPROT:P97178; EMBL:X97721; PIDN:CAA66307.1; PID:9178 C; Comment: This protein monomethylates residue A-2058 in 23S rRNA generating N6-methylated C; Genetics: A; Gene: tlrD C; Superfamily: rRNA (adenine-N6-) -methyltransferase

Query Match 18.1%; Score 67; DB 2; Length 481; Best Local Similarity 40.5%; Pred. No. 7, 3; Matches 15; Conservative 3; Mismatches 13; Indels 6; Gaps 1; R; Cole, S.T.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. C; Species: *Mycobacterium tuberculosis* Q; Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004 C; Accession: B70908 A; Status: preliminary; nucleic acid sequence not shown; translation not shown A; Molecule type: DNA A; Residues: 1-525 <COL> A; Cross-references: UNIPROT:Q10963; GB:Z74697; PIDN:CAA98978.

RESULT 4 JCS319 macrolide-lincomamide-streptogramin B resistance determinant - *Streptomyces fradiae* N; Alternative name: TLR protein C; Species: *Streptomyces fradiae* Q; Date: 01-May-1997 #sequence_revision 18-Jul-1997 #text_change 09-Jul-2004 C; Accession: JCS319 R; Gandeche, A.R.; Cundliffe, B. Gene 180, 173-176, 1996 A; Article: Molecular analysis of tlrD, an MLS resistance determinant from the tylosin producer *Streptomyces fradiae* A; Reference number: JCS319; MUID:9712823; PMID:8973363 A; Molecule type: DNA A; Residues: 1-27 <STR> A; Cross-references: UNIPROT:P97178; EMBL:X97721; PIDN:CAA66307.1; PID:9178 C; Comment: This protein monomethylates residue A-2058 in 23S rRNA generating N6-methylated C; Genetics: A; Gene: tlrD C; Superfamily: rRNA (adenine-N6-) -methyltransferase

Query Match 18.1%; Score 67; DB 2; Length 481; Best Local Similarity 40.5%; Pred. No. 7, 3; Matches 15; Conservative 3; Mismatches 13; Indels 6; Gaps 1; R; Cole, S.T.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. C; Species: *Mycobacterium tuberculosis* Q; Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004 C; Accession: D7047 A; Status: preliminary; nucleic acid sequence not shown; translation not shown A; Molecule type: DNA A; Residues: 1-525 <COL> A; Cross-references: UNIPROT:Q10963; GB:Z74697; PIDN:CAA98978.

RESULT 5 B70908 hypothetical protein Rv0591 - *Mycobacterium tuberculosis* C; Species: *Mycobacterium tuberculosis* Q; Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004 C; Accession: B70908 A; Status: preliminary; nucleic acid sequence not shown; translation not shown A; Molecule type: DNA A; Residues: 1-525 <COL> A; Cross-references: UNIPROT:Q10963; GB:Z74697; PIDN:CAA98978.

A;Experimental source: strain H37Rv
 C;Genetics:
 A;Gene: fhh
 C;Superfamily: signal recognition particle 54K protein
 Query Match Score 66; DB 2; Length 525;
 Best Local Similarity 45.2%; Pred. No. 10;
 Matches 19; Conservative 3; Mismatches 16; Indels 4; Gaps 3;
 Qy 19 PFLL--PRHTPYAGRNLG-FPESLGVPEFLPHFGGTRAPG 56
 Db 131 PLIVACDQLRPAVNQLQVGERAGVVFAPHFGASPDGPG 172

RESULT 8

S68470 Ca2+/Calmodulin-dependent protein kinase (EC 2.7.1.123) II beta-3 - rat
 C;Species: Rattus norvegicus (Norway rat)
 C;Date: 17-Jul-1998 #text_change 09-Jul-2004
 C;Accession: S68470; 153501
 R;Urquidi, V.; Ashcroft, S.J.H.
 P;BBS Lett. 358, 23-26, 1995
 A;Title: A novel pancreatic beta-cell isoform of calcium/calmodulin-dependent protein kinase
 A;Reference number: 153501; MUID:95121451; PMID:7821422
 A;Accession: S68470
 A;Molecule type: mRNA
 A;Residues: 1-589 <URO>
 A;Cross-references: UNIPROT:Q61094; EMBL:X83375; PID:96035
 A;Experimental source: pancreatic islets
 C;Complex: heteromultimer composed of 10-12 chains (alpha, beta, gamma, delta) generally
 C;Superfamily: Ca2+/Calmodulin-dependent protein kinase II; protein kinase homology
 C;Keywords: alternative splicing; ATP; autophosphorylation; calmodulin binding; phosphof
 P;12-272/Domain: protein kinase homology <KIN>
 P;20-28/Region: protein kinase ATP-binding motif
 P;43,51,134,138/Active site: Lys, Glu, Asp, Lys #status predicted
 P;287,306/Binding site: phosphate (Thr) (covalent) (by autophosphorylation) #status pred
 Query Match Score 66; DB 2; Length 589;
 Best Local Similarity 33.9%; Pred. No. 12;
 Matches 21; Conservative 3; Mismatches 18; Indels 20; Gaps 2;
 Qy 4 CLCRGAELSLCFSFPFLPLHTP-----VAGNVLGFPESLGVPEFLPHPGGTPRA 54
 Db 400 CLSPG-----LGPPLPSPSPRISDIILNSVRGSGTPBAGGPPVPPCPSPTL 448

RESULT 9

Qy 55 PG 56
 Db 449 PG 450

D70815 probable fadB protein - Mycobacterium tuberculosis (strain H37RV)
 C;Species: Mycobacterium tuberculosis
 C;Accession: D70815
 R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S
 ;Connor, R.; Davie, R.; Devlin, K.; Peltzwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.
 Rajanaream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
 Nature 393, 537-544, 1998
 A;Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
 A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
 A;Reference number: A70500; MUID:98235987; PMID:9634230
 A;Accession: D70815
 A;Status: Preliminary; nucleic acid sequence not shown; translation not shown
 A;Molecule type: DNA
 A;Residues: 1-720 <COL>
 A;Cross-references: UNIPROT:Q53872; GB:AL0220094; PID:93261550; MUID:CAA1766
 C;Genetics:
 A;Gene: fadB
 C;Superfamily: enoyl-CoA hydratase/3-hydroxyacyl-CoA dehydrogenase; 3-hydroxyacyl-CoA de

RESULT 10

E75447 hypothetical protein - Deinococcus radiodurans (strain R1)
 C;Species: Deinococcus radiodurans
 C;Accession: E75447
 R;White, O.; Elsen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
 M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma
 S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
 Science 286, 1571-1577, 1999
 A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
 A;Reference number: A75250; MUID:20036896; PMID:10567266
 A;Accession: E75447
 A;Status: Preliminary
 A;Molecule type: DNA
 A;Residues: 1-257 <WHI>
 A;Cross-references: UNIPROT:Q9RVL4; GB:AE001953; PID:96458740; PIDN:AAF1059
 A;Experimental source: strain R1
 C;Genetics:
 A;Gene: DR013
 A;Map position: 1

Query Match Score 65.5; DB 2; Length 257;
 Best Local Similarity 42.9%; Pred. No. 5.8;
 Matches 18; Conservative 1; Mismatches 18; Indels 5; Gaps 1;

Qy 17 FFPLLIPLHHTPVAGNVLGFPESLGVPEFLPHPGGTPRAGLIF 58
 Db 109 FFPLLIVLTLTGSVAGIHPGYG----EPRGGTGLGPGLF 145

RESULT 11

E72501 hypothetical protein APE1987 - Aeropyrum pernix (strain K1)
 C;Species: Aeropyrum pernix
 C;Accession: E72501
 R;Kawarabayashi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Tanaka, T.; Kudo, Y.; Yamazaki, J.; K
 awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Yamazaki, J.; K
 DNA Res. 6, 83-101, 1999
 A;Accession: E72501
 A;Status: Preliminary
 A;Molecule type: DNA
 A;Residues: 1-102 <WAV>
 A;Cross-references: UNIPROT:Q9YAF2; DDBJ:AP000063; PID:95105654; PIDN:BAA80997.1; PID:di
 A;Experimental source: strain K1
 C;Genetics:
 A;Gene: APE1987

Query Match Score 64.5; DB 2; Length 102;
 Best Local Similarity 43.2%; Pred. No. 3;
 Matches 16; Conservative 4; Mismatches 14; Indels 3; Gaps 2;

Qy 18 FPLLLP-LHPTPVAGNVLGFPESLGVPEFLPHPGGTP 52
 Db 29 YPLHAYPLLYKPGSSRGYGAAPPI-VPPGIVPHPNLPL 64

RESULT 12

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 29, 2005, 20:36:18 ; Search time 165 Seconds
 (without alignments)
 157.048 Million cell updates/sec

Title: US-10-649-857-45
 Perfect score: 371
 Sequence: 1 MGKCLCRGAEISLCSFPFL.....PGGTPRAPGLFLLFSEWAV 67

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Post-processing: Minimum Match 0% Maximum Match 100% Training Error 45.75%

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```
1: - geneseqP19300B:*
2: - geneseqP19300B:*
3: - geneseqP20015:*
4: - geneseqP20028:*
5: - geneseqP2003bs:*
6: - geneseqP2003bs:*
7: - geneseqP2003bs:*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, divided by the total number of results.

NUMBERS

Result No.	Score	Query	Match	Length	DB	ID	Description
1	371	100.0	67	2	AAW81944		Aaw81944 Human sec
2	371	100.0	150	2	AAY65459		Aay65459 Human nor
3	282	76.0	51	2	AAY83336		Aay83336 Human pro
4	76	20.5	126	4	AAO00972		Aao00972 Human REM
5	74.5	20.1	200	7	ADD65583		Add65583 Human REM
6	74.5	20.1	347	8	ADQ65482		Adq65482 Novel hum
7	73	19.7	200	8	ADR10217		Adr10217 Human pro
8	72	19.4	223	4	AAO00156		Aao00156 Human pol
9	71	19.1	135	4	AAU00562		Aau00562 Human pol
10	71	19.1	672	4	AAU28230		Aau28230 Novel hum
11	71	19.1	672	4	AAU28232		Aau28232 Novel hum
12	71	19.1	672	4	AAU28231		Aau28231 Novel hum
13	70.5	19.0	142	4	AAO00501		Aao00501 Human pol
14	69	18.6	107	4	ABG12930		Abg12930 Novel hum
15	67	18.1	100	5	AKD34374		Akd34374 Novel hum
16	67	18.1	117	4	AAO13083		Aao13083 Human pol
17	67	18.1	481	5	ABJ01679		Abj01679 Mycobacte
18	66.5	17.9	142	7	ADB64520		Adb64520 Human pro
19	66.5	17.9	461	5	ADK34685		Adk34685 Novel hum
20	66.5	17.9	806	6	ABO01125		Abo01125 Novel hum
21	66	17.8	131	4	AAO04859		Aao04859 Human pol
22	66	17.8	179	4	ABG18182		Abg18182 Novel hum
23	66	17.8	517	6	ABU34062		Abu34062 Protein e
24	66	17.8	525	6	ABU34661		Abu34661 Protein e
25	66	17.8	525	6	ABU16878		Abu16878 Protein e

226	66	17.8	712	6	ABU34588	Protein e
227	66	17.8	720	6	ABU36338	Protein e
228	65.5	17.7	135	4	AA001708	Human pol
229	65	17.5	7	7	AD121224	Novel hum
330	65	17.5	422	4	ABG22390	Novel hum
331	65	17.5	452	8	ADG066221	Novel hum
332	64.5	17.4	130	4	AA001554	Human pol
333	64.5	17.4	424	8	ADG22716	Cyanophag
334	64.5	17.4	426	7	ABO65478	Klebsiell
335	64.5	17.4	692	6	ABU28111	Protein e
336	64	17.3	106	4	AA0017378	Human pol
337	64	17.3	320	5	AAU78461	Mouse bet
338	64	17.3	413	7	ADJ8115	Ovine con
339	64	17.3	521	6	ABU35572	Protein e
410	64	17.3	1494	5	AAU78460	Mouse bet
411	63.5	17.1	123	4	AA004222	Human pol
442	63.5	17.1	336	7	ADB63875	Human pro
443	63.5	17.1	710	6	ABU41050	Protein e
444	63.5	17.1	724	6	ABU45290	Protein e
445	63.5	17.1	731	7	ADF03896	Bacterial

ALIGNMENTS

XX AAW83944;
AC XX 28-JAN-1999 (first entry)
XX DT XX

Wien. Ber.

XX	Key	Location/Qualifie
FH	Peptide	1. .32
FT		/note= "signal pe
FT	Protein	33. :67
FT		/note= "mature se
XX		
PN		W09845712-A2.

PD	15-PTD-1998.
XX	07-APR-1998;
XX	08-APR-1997;
PR	30-MAY-1997;
PR	30-MAY-1997;
PR	30-MAY-1997;
XX	98WO-US006801.
PA	(HUMA-) HUMAN GENOME SCI INC.
XX	Rosser CA, Ruben SM, Yu G, Ni J
PI	WPI: 1998-594496/50.
XX	N-PSDB; AAV69524.
DR	DR

PT New isolated human genes and secreted polypeptide(s) they encode - useful for the diagnosis and treatment of e.g. cancers, CNS disorders, immune system disorders, inflammatory disease and bacterial infections.

PT XX

XX Claim 11; Page 123: 142pp; English.

CC This sequence represents a human secreted protein encoded by a nucleic acid molecule designated Gene 14 from the human cDNA clone HNGBV36 (deposited as clone ARCC 97955 and ARCC 209704). The gene is expressed primarily in breast cancer, pituitary and activated T cells and to a lesser extent in frontal cortex and breast and is useful for diagnosis and treatment of breast cancer and growth disorders. The invention relates to 20 novel genes and their fragments (AAV69611 to AAV69630) and corresponding secreted proteins (AAW83911 to AAW83950) which are useful for preventing, treating or ameliorating medical conditions e.g. by protein of gene therapy. Also pathological conditions can be diagnosed by determining the amount of the new polypeptides in a sample or by determining the presence of mutations in the polymucleotides. Specific uses are based on which tissues they are most highly expressed in, and include developing products for the diagnosis or treatment of central nervous system (CNS) and immune system diseases, reproductive disorders, cancers, congenital malformations, degenerative diseases, trauma, inflammatory disease, neoplasia, metabolic disorders, diseases in testes, placenta, liver, brain and activated T cells, spleen diseases, lung diseases, heart diseases, rhabdomyosarcoma and disorders of the endocrine system or other endocrinopathies, e.g. endocrine polylglandular syndrome, endocrinoma, and endocrine ophthalmopathy, osteoclastoma and other bone remodelling disorders, bacterial infections and sepsis. The polypeptides are also useful for identifying their binding partners

XX Sequence 67 AA;

Query Match 100.0%; Score 371; DB 2; Length 67;

Best Local Similarity 100.0%; Pred. No. 1.8e-34; Matches 67; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGKCLCRGAELSLCFSFPFLPLPLTPVAGRNLFPESLGVPPFLPHPGTTPRAGLFL 60
Db 1 MGKCLCRGAELSLCFSFPFLPLPLTPVAGRNLFPESLGVPPFLPHPGTTPRAGLFL 60

RESULT 3
AAV48336

ID AAV48336 standard; protein; 51 AA.

XX

AC AAV48336;

XX DT 08-DEC-1999 (first entry)

XX DE Human prostate cancer-associated protein 33.

XX KW Expressed sequence tag; EST; prostate; tumor; treatment; gene therapy; Homo sapiens.

XX OS Homo sapiens.

XX PN DE19811194-A1.

XX PD 16-SEP-1999.

XX XX 98DB-01011194.

XX PF 10-MAR-1998;

XX PR 10-MAR-1998;

XX DR 98DB-01011194.

XX PA (META-) METAGEN GES GENOMFORSCHUNG MBH.

XX Specht T, Hinzmann B, Schmitt A, Pilarsky C, Dahl E, Rosenthal A;

XX PI XX

DR WPI; 1999-519629/44.

XX DR N-PSDB; AAZ33494.

XX PT New nucleic acid expressed at high level in normal prostatic tissue and encoded polypeptides, used to treat cancer and screen for therapeutic agents.

XX DR WPI; 1999-602416/52.

DR N-PSDB; AAZ42232.
XX
PT New polypeptides and their nucleic acids, useful for treatment of bladder tumor and identification of therapeutic agents.

XX Claim 23; Page 334; 366pp; German.

CC This invention describes novel polypeptide fragment sequences (I) and (II) which are highly expressed in normal bladder tissue and have cytostatic activity. (III) are used for recombinant expression of (I) and to isolate complete genes. (I) are used to identify agents suitable for the treatment of bladder tumours, to directly treat this form of cancer (including expression from gene therapy vectors), or are used in a preparation for cancer treatment. (I) are also used for the generation of specific antibodies. (II) are identified by assembling ESTs (expressed sequence tags) from a particular tissue type before comparison of expression patterns. This allows a significantly longer fragment of the gene to be revealed, and therefore reduces the number of failures because of ESTs from different libraries representing different parts of the same unknown gene distorting the estimated frequency of occurrence in a particular tissue. AAY6329-Y60591 represent protein fragments encoded in a preparation for cancer treatment by the human normal bladder tissue cDNA library derived EST fragments represented in AAZ42122-Z42248 Sequence 150 AA;

Query Match 100.0%; Score 371; DB 2; Length 150;

Best Local Similarity 100.0%; Pred. No. 4e-34; Matches 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGKCLCRGAELSLCFSFPFLPLPLTPVAGRNLFPESLGVPPFLPHPGTTPRAGLFL 60
Db 84 MGKCLCRGAELSLCFSFPFLPLPLTPVAGRNLFPESLGVPPFLPHPGTTPRAGLFL 143
Qy 61 LFSFWAV 67
Db 144 LFSFWAV 150

RESULT 3

AAV48336

ID AAV48336 standard; protein; 51 AA.

XX

AC AAV48336;

XX DT 08-DEC-1999 (first entry)

XX DE Human prostate cancer-associated protein 33.

XX KW Expressed sequence tag; EST; prostate; tumor; treatment; gene therapy; Homo sapiens.

XX OS Homo sapiens.

XX PN DE19811194-A1.

XX PD 16-SEP-1999.

XX XX 98DB-01011194.

XX PF 10-MAR-1998;

XX PR 10-MAR-1998;

XX DR 98DB-01011194.

XX PA (META-) METAGEN GES GENOMFORSCHUNG MBH.

XX Specht T, Hinzmann B, Schmitt A, Pilarsky C, Dahl E, Rosenthal A;

XX PI XX

DR WPI; 1999-519629/44.

XX DR N-PSDB; AAZ33494.

XX PT New nucleic acid expressed at high level in normal prostatic tissue and encoded polypeptides, used to treat cancer and screen for therapeutic agents.

PS Claim 22; 137; 194pp; German.

XX This invention describes novel nucleic acid sequences (A) that are expressed at high level in normal prostatic tissue. Polypeptides (I) encoded by (A) are used: (a) for identity testing agents for treatment of prostatic cancer and (b) for therapy of prostate cancer, optionally where expressed by gene therapy methods. (A) is also used to isolate full-length genes (for gene therapy) and for recombinant production of (I), which can be used to raise specific antibodies. (A) are identified by assembly of ESTs (expressed sequence tags) before these are analyzed for expression pattern (tissue specificity). This approach eliminates many of the false results, as regards tissue specificity, associated with known methods that use single (usually short) ESTs. AY48304-Y48356 represent peptides encoded by the expressed sequence tags described in the method of the invention

XX Sequence 51 AA;

Query Match 76.0%; Score 282; DB 2; Length 51;
Best Local Similarity 100.0%; Pred. No. 1.7e-24;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 17 FPLPLPLHTPVAGRNLFPESLGVPPLPHGGTPRAAGFLFLLFSWAV 67
Db 1 FPLPLPLHTPVAGRNLFPESLGVPPLPHGGTPRAAGFLFLLFSWAV 51

XX RESULT 4

AA000972 Human polypeptide SEQ ID NO 14864.
XX

KW Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haemopoiesis; KW tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorders; arthritis; inflammation.
XX Homo sapiens.
OS WO200164835-A2.
PN 07-SEP-2001.

XX

PR 26-FEB-2001; 2001WO-US004927.
PR 28-FEB-2000; 2000US-00515126.
PR 18-MAY-2000; 2000US-00577409.

XX

PA (HYSE-) HYSQ INC.

XX Tang YT, Liu C, Drmanac RT;
XX DR-2001-514838156.
XX N-PSDB; AAI89093.

PT Isolated nucleic acids and polypeptides, useful for preventing diagnosing and treating e.g. leukemia, inflammation and immune disorders.
XX

PS Claim 20; SEQ ID NO 14864; 139pp + Sequence Listing; English.

CC The invention relates to human polynucleotides (AAI79941-AAI93841) and the encoded proteins (AA00010-AA013910) that exhibit activity relating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haemopoiesis regulating activity, tissue growth factor activity, immunomodulatory activity and

CC activation/inhibitory activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and/or inflammation. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 126 AA;

Query Match 20.5%; Score 76; DB 4;
Best Local Similarity 37.9%; Pred. No. 1.1;
Matches 22; Conservative 3; Mismatches 21; Indels 12; Gaps 3;

Qy 18 FPLPLPLHTPVAGRNLFPESLGVPPLPHGGTPRAAGFLFLLFSW 64
Db 8 FP-LsLyTPHGHGSGPPTGAGCPAPPARKSHQKVGRQKGPFGVPPRPAFLFFF 64

XX RESULT 5

ADD65583 ID ADD65583 standard; protein; 200 AA.
XX AC ADD65583;
XX DT 15-JAN-2004 (first entry)
XX DS Human REMAP protein - SEQ ID 12.
XX KW human; receptor and membrane-associated protein; REMAP; cytosolic;
KW antiarteriosclerotic; anticonvulsant; nootropic; neuroprotective;
KW cerebroprotective; anti-HIV; antiallergic; antiinflammatory;
KW thymomimetic; cell proliferative; cancer; atherosclerosis; neurological;
KW epilepsy; Huntington's disease; stroke; immune; inflammatory; AIDS;
KW allergy; developmental; hypothyroidism; Cushing's syndrome; infection.
XX OS Homo sapiens.
XX PN WO2003048305-A2.
XX PD 12-JUN-2003.
XX PP 13-NOV-2002; 2002WO-US036759.
XX PR 13-NOV-2001; 2001US-03331097P.
XX PR 15-NOV-2001; 2001US-033274P.
XX PR 14-DEC-2001; 2001US-034542P.
XX PR 18-DEC-2001; 2001US-0342166P.
XX PR 11-JAN-2002; 2002US-034580P.
XX PR 14-JAN-2002; 2002US-034687P.
XX PA (INCYT-) INCYTE GENOMICS INC.

XX Duggan BM, Yang J, Gietzen KJ, Lee SY, Tang YT, Azimzai Y;
PI Chawla NK, Warren BA, Barroso I, Becha SD, Rue H, Lehr-Mason PM;
PI Thangavelu K, Lee S, Emerling BM, Khare R, Baughn MR;
PI Gandhi AR, Tran UK, Richardson TW, Marquis JP, Lal PG, Forsythe IJ;
PI Lee EA, Swarbrick A, Kallick DA, Griffin JA, Gorvad AE;
PI Hafalia AJA, Ison CH, Jin P, Jiang X, Jackson AA, Bhatia U;
PI Burkill JD, Blake JJ, Ho A, Zheng W, Gao J;
XX DR WPI; 2003-513744/48.
XX DR N-PSDB; ADD69330.

PT New human receptors and membrane-associated proteins (REMAP), useful for diagnosing, treating and preventing diseases or conditions associated with the aberrant REMAP expression e.g. cancer, AIDS, atherosclerosis, or infections.

XX Claim 1; SEQ ID NO 12; 298pp; English.

CC The invention relates to a novel polypeptide comprising a human receptor and membrane-associated protein (REMAP), the polypeptide of the invention demonstrates cytotatic, antiarteriosclerotic, anticonvulsant, nootropic, neuroprotective, cerebroprotective, anti-HIV, antiallergic,

Qy	17 FPPPLPLPLHT--PVAGRNLLGFPEPSLGPVPPFLPHPGGTPR-APGLFLLLPSFW 65	XX	06-NOV-2001 (first entry)
Db	130 FSEPCIPHSPPVEG--GAPGSPSPVPHLTHTLGPRLLPGALTDPAEW 178	XX	Human polypeptide SEQ ID NO 15454.
RESULT 8		XX	
ID AAO06156	standard; protein; 223 AA.	XX	Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haemopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorders; arthritis; inflammation.
XX		XX	
AC AAO06156;		OS	Homo sapiens.
XX		XX	
DT 06-NOV-2001	(first entry)	XX	WO200164835-A2.
DE Human polypeptide SEQ ID NO 20048.		XX	07-SEP-2001.
XX		XX	XX
KW Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haemopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorders; arthritis; inflammation.		XX	26-FEB-2001; 2001WO-US004927.
XX		XX	XX
OS Homo sapiens.		XX	28-FEB-2000; 2000US-00515126.
XX		XX	PR 18-MAY-2000; 2000US-00577409.
PN WO200164835-A2.		XX	XX
XX		XX	XX
PD 07-SEP-2001;		XX	PA (HYSEQ -) HYSEQ INC.
XX		XX	XX
PP 26-FEB-2001; 2001WO-US004927.		XX	PI Tang YT, Liu C, Drmanac RT;
XX		XX	XX
PR 28-FEB-2000; 2000US-00515126.		XX	DR WPI; 2001-514838/56.
XX		XX	XX
PR 18-MAY-2000; 2000US-00577409.		XX	PT Isolated nucleic acids and polypeptides, useful for preventing diagnosing and treating e.g. leukemia, inflammation and immune disorders.
XX		XX	XX
PA (HYSEQ INC.		XX	CC Claim 20; SEQ ID NO 15454; 1399pp + Sequence Listing; English.
XX		XX	CC The invention relates to human polynucleotides (AAI79941-AAI93841) and the encoded proteins (AA00010-AAI3910) that exhibit activity relating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haemopoiesis regulating activity, tissue growth factor activity, immunomodulatory activity and activity/inhibitory activity and may be useful in the diagnosis and/or treatment of cancer, leukemia, nervous system disorders, arthritis and inflammation. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
PI Tang YT, Liu C, Drmanac RT;		XX	CC sequence 135 AA;
XX		XX	CC Query Match 19.1%; Score 71; DB 4; Length 135;
DR WPI; 2001-514838/56.		XX	CC Best Local Similarity 36.4%; Pred. No. 4.2; Mismatches 5;
DR N-PSDB; AA186087.		XX	CC Matches 24; Conservative 4; Mismatches 22; Indels 16; Gaps 5;
XX		XX	CC
PT Isolated nucleic acids and polypeptides, useful for preventing diagnosing and treating e.g. leukemia, inflammation and immune disorders.		XX	CC
XX		XX	CC
PS Claim 20; SEQ ID NO 20048; 1399pp + Sequence Listing; English.		XX	CC
XX		XX	CC
CC The invention relates to human polynucleotides (AAI79941-AAI93841) and the encoded proteins (AA00010-AAI3910) that exhibit activity relating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haemopoiesis regulating activity and activity/inhibitory activity and may be useful in the diagnosis and/or treatment of cancer, leukemia, nervous system disorders, arthritis and inflammation. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences		CC	
CC Sequence 223 AA;		XX	CC
CC Query Match 19.4%; Score 72; DB 4; Length 223;		XX	CC
CC Best Local Similarity 45.5%; Pred. No. 5.4; Mismatches 0; Indels 8; Gaps 1;		XX	CC
CC Matches 15; Conservative 15; Mismatches 10; Indels 8; Gaps 1;		XX	CC
XX		XX	CC
Qy 23 PFLFPLPLPLHT--PVAGRNLLGFPEPSLGPVPPFLPHPGGTPR-APGLFLLLPSFW 55		XX	CC RESULT 10
Db 121 PSHVP-----PHPLAFFFGEKFKPFLAPGGA--GGLFSFPEASSPGLNPFWPNPDKKKGPP 145		XX	AAU28230
RESULT 9		XX	ID AAU28230 standard; protein; 672 AA.
AA001562		XX	ID Novel human secretory protein, Seq ID No 587.
ID AAO01562 standard; protein; 135 AA.		XX	AC AAU28230;
XX		XX	AC Human; secreted protein; arthritis; Crohn's disease; sepsis; shock;
AC AAO01562;		XX	DT 18-DEC-2001 (first entry)

CC activity, regulation of haematopoiesis and is useful for treating myeloid
 CC or lymphoid cell disorders, platelet disorders such as thrombocytopenia
 CC and for regeneration of bone, cartilage, tendon, ligament and/or nerve
 CC tissue growth, and in tissue repair, healing of burns, incisions, ulcers,
 CC or periodontal disease. Furthermore, (I) is also useful for gut
 CC protection or regeneration and treatment of lung or liver fibrosis,
 CC reperfusion injury in various tissues, various immune deficiencies and
 CC disorders including severe combined immunodeficiency (SCID), bacterial or
 CC fungal infections, autoimmune disorders e.g. multiple sclerosis,
 CC rheumatoid arthritis, diabetes mellitus, myasthenia gravis, allergic
 CC reactions and conditions, such as asthma or other respiratory problems.
 CC In addition, (I) affects biorhythms or circadian cycles of rhythms,
 CC fertility, metabolism, carbohydrate, vitamins, minerals, provides
 CC dietary fat, lipid, protein, carbohydrate, vitamins, minerals, provides
 CC analgesic effects or other pain reducing effects, immunoglobulin like
 CC activity and can act as an antigen in a vaccine composition to raise an
 CC immune response. AAU8020-AAU28395 represent novel human secreted protein
 XX amino acid sequences of the invention.

SQ Sequence 672 AA;

Query Match 19.1%; Score 71; DB 4; Length 672;
 Best Local Similarity 40.7%; Pred. No. 21;
 Matches 22; Conservative 1; Mismatches 17; Indels 14; Gaps 3;
 AC AAU2831;
 DT 18-DEC-2001 (first entry)

Dbb 589 PLQLPFHPPPLGLACGFLLPSSVGGFVPCFLGAQSGAWHIFPRPTAF 642

RESULT 12

AAU2831 standard; protein; 672 AA.

XX Human; secreted protein; arthritis; Crohn's disease; sepsis; shock;

XX ischaemia-reperfusion injury; haematopoiesis; cancer; neuropathy;

XX transgenic animal; Alzheimer's disease; Parkinson's disease; burn;

XX amytrophic lateral sclerosis; platelet disorder; thrombocytopenia;

XX ulcer; osteoporosis; bone degenerative disorder; periodontal disease;

XX gut protection; lung; liver fibrosis; immune deficiency; infection;

XX severe combined immunodeficiency; SCID; autoimmune disorder; allergy;

XX multiple sclerosis; rheumatoid arthritis; diabetes mellitus; asthma;

XX fertility; analgesic; pain; antigen.

OS Homo sapiens.

PN WO200166689-A2.

XX 13-SEP-2001.

XX 05-MAR-2001; 2001WO-US004942.

XX 07-MAR-2000; 2000US-00519705.

PR 19-MAY-2000; 2000US-00574454.

PR 17-JUN-2000; 2000US-00596193.

PR 14-JUL-2000; 2000US-00616347.

PR 19-SEP-2000; 2000US-00665313.

PR 20-OCT-2000; 2000US-00693267.

XX (HYSE-) HYSEQ INC.

PI Tang YT, Liu C, Asundi V, Xu C, Wehrman T, Ren F, Ma Y, Zhou P;

PI Zhao QA, Yang Y, Drmanac RT, Zhang J, Chen R, Xue AJ, Wang J;

DR WPI; 2001-589934/66.

N-PSDB; AAS45131.

XX

PT prepared from various human tissues.

PT cancer, neurological, inflammatory, and autoimmune disorders.

XX

PS

Example 2; SEQ ID NO 588; 107PP; English.

The invention relates to novel isolated human secreted polypeptides (I)

CC and polynucleotides (III). (I) and (II) are useful for treating

CC inflammatory conditions such as arthritis, nephritis, Crohn's disease,

CC ischaemia-reperfusion injury, shock, sepsis, immune responses, and is

CC involved in increasing haemopoiesis, stem cell survival, bone growth

CC and remodelling. (I), (II) and modulators of (III) are useful for

CC prophylaxis or treatment of one or more cancers. (II) is also useful for

CC creating transgenic animals useful for studying the in vivo activities of

CC the polypeptide as well as for studying modulators of the polypeptides.

CC (I) induces the proliferation of neural cells and regeneration of nerve

CC and brain tissue and is useful for the treatment of central and

CC peripheral nervous system diseases and neuropathies, such as Alzheimer's,

CC Parkinson's disease, Huntington's disease, and amyotrophic lateral

CC sclerosis. In addition, (I) is involved in chemotactic or chemokinetic

CC activity, regulation of haemopoiesis and is useful for treating myeloid

CC or lymphoid cell disorders, platelet disorders such as thrombocytopenia

CC and for regeneration of bone, cartilage, tendon, ligament and/or nerve

CC tissue growth, and in tissue repair, healing of burns, incisions, ulcers,

CC for treating osteoporosis, osteoarthritis, bone degenerative disorders,

CC or periodontal disease. Furthermore, (I) is also useful for gut

CC protection or regeneration and treatment of lung or liver fibrosis,

CC disorders including severe combined immunodeficiency (SCID), bacterial or

CC fungal infections, autoimmune disorders e.g. multiple sclerosis, and

CC various immune deficiencies and

CC disorders including severe combined immunodeficiency (SCID), bacterial or

CC fungal infections, autoimmune disorders mellitus, myasthenia gravis, allergic

CC reactions and conditions, such as asthma or other respiratory problems.

CC In addition, (I) affects biorhythms or circadian cycles of rhythms,

CC fertility, metabolism, catabolism, anabolism, storage or elimination of

CC dietary fat, lipid, protein, carbohydrate, vitamins, minerals, provides

CC analgesic effects or other pain reducing effects, immunoglobulin like

CC activity and can act as an antigen in a vaccine composition to raise an

CC immune response. AAU28010-AAU28395 represent novel human secreted protein

XX

SQ Sequence 672 AA;

Query Match 19.1%; Score 71; DB 4; Length 672;

Best Local Similarity 40.7%; Pred. No. 21;

Matches 22; Conservative 1; Mismatches 17; Indels 14; Gaps 3;

Qy 19 PLPLPLHTPVAGRNLF--PBSLGI-----PRAPGLF 58

Db 589 PLQLPFHPPPLGLACGFLLPSSVGGFVPCFLGAQSGAWHIFPRPTAF 642

XX

Sequence 672 AA;

SQ

RESULT 13

AA000501

ID AA000501 standard; protein; 142 AA.

XX

AC AA000501;

XX

AC AA000501;

XX

DT DT

XX

06-NOV-2001 (first entry)

XX

Human polypeptide SEQ ID NO 14393.

DB DB

XX

Human; cytokine; cell proliferation; cell differentiation; gene therapy;

KW KW

vaccine; peptide therapy; stem cell growth factor; haematoopoiesis;

KW KW

tissue growth factor; immunomodulatory; cancer; leukaemia;

KW KW

nervous system disorders; arthritides; inflammation.

XX

Homo sapiens.

XX

PN WO200164835-A2.

XX

PD PD

07-SEP-2001.

XX

07-SEP-2001.

PP 26-FEB-2001; 2001WO-US004927.
 XX PT New isolated polynucleotide and encoded polypeptides, useful in
 PR PT diagnostics, forensics, gene mapping, identification of mutations
 PR PT responsible for genetic disorders or other traits and to assess
 XX PT PT biodiversity.
 XX XX
 PA PS Claim 20, SEQ ID NO 43289; 103pp; English.
 XX
 PI Tang YT, Liu C, Drmanac RT;
 XX WPI; 2001-514838/56.
 DR N-PSDB; AAI80432.
 XX
 PT Isolated nucleic acids and polypeptides, useful for preventing diagnosing
 PT and treating e.g. leukemia, inflammation and immune disorders.
 XX PS Claim 20, SEQ ID NO 14393; 139pp + Sequence Listing; English.
 XX
 CC The invention relates to human polynucleotides (AAI79941-AAI93841) and
 CC the encoded Proteins (AA00010-AA013910) that exhibit activity relating to
 CC cytokine, cell proliferation or cell differentiation or which may induce
 CC production of other cytokines in other cell populations. The
 CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
 CC peptide therapy. The polypeptides have various cytokine-like activities,
 CC e.g. stem cell growth factor activity, haemomodulatory activity and
 CC activity, tissue growth factor activity, immunomodulatory activity and
 CC activin/inhibin activity and may be useful in the diagnosis and/or
 CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
 CC inflammation. Note: The sequence data for this patent did not form part
 CC of the printed specification, but was obtained in electronic format
 CC directly from WIPO at ftp://wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 142 AA;
 Query Match Score 70.5%; DB 4; Length 142;
 Best Local Similarity 37.3%; Pred. No. 5.1;
 Matches 19; Conservative 1; Mismatches 20; Indels 11; Gaps 2;
 Qy 19 PLLPLPH-----TPVAGRNLGFPESTLGVPPF-----LPHPGGTTPRAGLFL 58
 Db 29 PUSPPWGSKEVVPXVKGRBLPGXAGKPPPEFLKEQFPFRGGGBRCPPFL 79
 RESULT 14
 ABG12930
 ID ABG12930 standard; protein; 107 AA.
 XX AC ABG12930;
 XX DT 13-FEB-2002 (first entry)
 DE Novel human diagnostic protein #12921.
 XX Human; chromosome mapping; Gene mapping; gene therapy; forensic;
 KW food supplement; medical imaging; diagnostic; genetic disorder.
 XX Homo sapiens.
 OS WO200175057-A2.
 PN 11-OCT-2001.
 XX PF 30-MAR-2001; 2001WO-US008631.
 XX PR 31-MAR-2000; 2000US-00549217.
 XX PR 23-AUG-2000; 2000US-00649167.
 XX PA (HYSEQ INC.
 PI Drmanac RT, Liu C, Tang YT;
 XX WPI; 2001-639362/73.
 DR N-PSDB; AAS77117/73.
 XX
 PT Key Location/Qualifiers
 PT Misc-difference 1 .100
 PT /label= OTHER
 PT /note= "OTHER= All xaa's in this sequence are unknown
 amino acids or the site of a stop codon within the DNA
 sequence"
 PT XX WO200216439-A2.
 PT XX
 PT PD 28-FEB-2002.
 PT XX
 PT PD 28-FEB-2002.

XX
PP 05-MAR-2001; 2001WO-US004941.
XX
PR 07-MAR-2000; 2000US-00519705.
PR 19-MAY-2000; 2000US-00574454.
XX
PA (HYSEQ) HYSEQ INC.
XX
PI Tang YT, Liu C, Drmanac RT;
XX
DR WPI; 2002-280918/32.
XX
PT Isolated polynucleotide encoding bone marrow derived polypeptides useful
PT for treating, e.g., Parkinson's, Alzheimer's, cancer, arthritis, Crohn's
PT disease, and inflammatory bowel disease.
XX
PS Claim 20, SEQ ID NO 6456; 504PD; English.
XX
CC This invention relates to a novel isolated polynucleotide comprising a
CC nucleotide sequence selected from one of 1680 sequences, a mature protein
CC coding portion of them, an active domain of them and their complementary
CC sequences. The invention may be useful for the production of compounds
CC with an antiarthritic, antiparkinsonian, neuroprotective, nootropic,
CC immunosuppressive, cytostatic, antipsoriatic, antinflammatory,
CC antibacterial, antiviral, antifungal or antiparasitic activity. In
CC addition, the disclosed sequences may be useful for gene therapy. The
CC polypeptides or their antibodies are useful for treating many diseases
CC such as arthritis, Parkinson's, Alzheimer's, autoimmune diseases, cancer,
CC psoriasis, inflammatory bowel disease and infections caused by bacteria,
CC viruses, fungi or parasites. The present sequence is that of a human,
CC polypeptide of the invention.
XX
SQ Sequence 100 AA:
XX

Query Match 18.1%; Score 67; DB 5; Length 100;
Best Local Similarity 40.4%; Pred. No. 8.9;
Matches 21; Conservative 1; Mismatches 16; Indels 14; Gaps 3;
Qy 17 FFPILLPLIHTPVAGRNLGFPBESLGVV-----PFLDHPGG-TPRAGLFL 60
Db 18 FPPQRAFTNP-----LGPPGGLGPNNPPRGFPFPGKPPPKNGFFFL 63

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